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(54) Title: SEED TRAIT GENES

(57) Abstract: Recombinant polynucleotides and methods for modifying the phenotype of a plant are provided. In particular, the phenotype that is being modified is a plant's seed characteristics.

SEED TRAIT GENES

RELATED APPLICATION INFORMATION

The present invention claims the benefit from US Provisional Patent Application Serial Nos. 60/166,228 filed November 17, 1999 and 60/197,899 filed April 17, 2000 and "Plant Trait Modification III" filed August 22, 2000.

FIELD OF THE INVENTION

This invention relates to the field of plant biology. More particularly, the present invention pertains to compositions and methods for phenotypically modifying a plant.

BACKGROUND OF THE INVENTION

Transcription factors can modulate gene expression, either increasing or decreasing (inducing or repressing) the rate of transcription. This modulation results in differential levels of gene expression at various developmental stages, in different tissues and cell types, and in response to different exogenous (e.g., environmental) and endogenous stimuli throughout the life cycle of the organism.

Because transcription factors are key controlling elements of biological pathways, altering the expression levels of one or more transcription factors can change entire biological pathways in an organism. For example, manipulation of the levels of selected transcription factors may result in increased expression of economically useful proteins or metabolic chemicals in plants or to improve other agriculturally relevant characteristics. Conversely, blocked or reduced expression of a transcription factor may reduce biosynthesis of unwanted compounds or remove an undesirable trait. Therefore, manipulating transcription factor levels in a plant offers tremendous potential in agricultural biotechnology for modifying a plant's traits.

The present invention provides novel transcription factors useful for modifying a plant's phenotype in desirable ways, such as modifying the characteristics of a plant's seed.

SUMMARY OF THE INVENTION

In a first aspect, the invention relates to a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-27, or a complementary nucleotide sequence thereof; (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a); (c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-1, where N=1-27, or a

complementary nucleotide sequence thereof; (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c); (e) a nucleotide sequence which hybridizes under stringent conditions over substantially the entire length of a nucleotide sequence of one or more of: (a), (b), (c), or (d); (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e); (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide having a biological activity that modifies a plant's seed characteristics; (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g); (i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g); (j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27; (k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27; and (l) a nucleotide sequence which encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-27. The recombinant polynucleotide may further comprise a constitutive, inducible, or tissue-active promoter operably linked to the nucleotide sequence. The invention also relates to compositions comprising at least two of the above described polynucleotides.

In a second aspect, the invention is an isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide described above.

In another aspect, the invention is a transgenic plant comprising one or more of the above described recombinant polynucleotides. In yet another aspect, the invention is a plant with altered expression levels of a polynucleotide described above or a plant with altered expression or activity levels of an above described polypeptide. Further, the invention may be a plant lacking a nucleotide sequence encoding a polypeptide described above. The plant may be a soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, or vegetable brassicas plant.

In a further aspect, the invention relates to a cloning or expression vector comprising the isolated or recombinant polynucleotide described above or cells comprising the cloning or expression vector.

In yet a further aspect, the invention relates to a composition produced by incubating a polynucleotide of the invention with a nuclease, a restriction enzyme, a polymerase; a polymerase and a primer; a cloning vector, or with a cell.

Furthermore, the invention relates to a method for producing a plant having improved seed traits. The method comprises altering the expression of an isolated or recombinant polynucleotide of the invention or altering the expression or activity of a polypeptide of the invention in a plant to produce a modified plant, and selecting the modified plant for modified seed traits.

In another aspect, the invention relates to a method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of the invention. The method comprises expressing a polypeptide encoded by the polynucleotide in a plant; and identifying at least one factor that is modulated by or interacts with the polypeptide. In one embodiment the method for identifying modulating or interacting factors is by detecting binding by the polypeptide to a promoter sequence, or by detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system, or by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.

In yet another aspect, the invention is a method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest. The method comprises placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of the invention and monitoring one or more of the expression level of the polynucleotide in the plant, the expression level of the polypeptide in the plant, and modulation of an activity of the polypeptide in the plant.

In yet another aspect, the invention relates to an integrated system, computer or computer readable medium comprising one or more character strings corresponding to a polynucleotide of the invention, or to a polypeptide encoded by the polynucleotide. The integrated system, computer or computer readable medium may comprise a link between one or more sequence strings to a modified plant seed trait.

In yet another aspect, the invention is a method for identifying a sequence similar or homologous to one or more polynucleotides of the invention, or one or more polypeptides encoded by the polynucleotides. The method comprises providing a sequence database; and, querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences.

The method may further comprise of linking the one or more of the polynucleotides of the invention, or encoded polypeptides, to a modified plant seed characteristics phenotype.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 provides a table of exemplary polynucleotide and polypeptide sequences of the invention. The table includes from left to right for each sequence: the SEQ ID No., the internal code reference number (GID), whether the sequence is a polynucleotide or polypeptide sequence, and identification of any conserved domains for the polypeptide sequences.

Figure 2 provides a table of exemplary sequences that are homologous to other sequences provided in the Sequence Listing and that are derived from *Arabidopsis thaliana*. The table includes from left to right: the SEQ ID No., the internal code reference number (GID), identification of the homologous sequence, whether the sequence is a polynucleotide or polypeptide sequence, and identification of any conserved domains for the polypeptide sequences.

Figure 3 provides a table of exemplary sequences that are homologous to the sequences provided in Figures 1 and 2 and that are derived from plants other than *Arabidopsis thaliana*. The table includes from left to right: the SEQ ID No., the internal code reference number (GID), the unique GenBank sequence ID No. (NID), the probability that the comparison was generated by chance (P-value), and the species from which the homologous gene was identified.

DETAILED DESCRIPTION

The present invention relates to polynucleotides and polypeptides, e.g. for modifying phenotypes of plants.

In particular, the polynucleotides or polypeptides are useful for modifying traits associated with a plant's seed characteristics when the expression levels of the polynucleotides or expression levels or activity levels of the polypeptides are altered. Specifically, the polynucleotides and polypeptides are useful for modifying the nutritional content or composition of seeds: such as to modify the protein or oil content of seeds, to modify insoluble sugar content or composition, such as by altering the levels of arabinose, fucose, galactose, mannose, rhamnose or xylose or the like; modify prenyl lipid content or composition, such as by altering the levels of lutein, beta-carotene, xanthophyll-1, xanthophyll-2, chlorophylls A or B, or alpha-, delta- or gamma-tocopherol or the like; modify fatty acid content or composition, such as by altering the levels of the fatty acids 16:0 (palmitic acid), 16:1 (palmitoleic acid), 18:0 (stearic acid), 18:1

(oleic acid), 18:2 (linoleic acid), 20:0 , 18:3 (linolenic acid), 20:1 (eicosenoic acid), 20:2 and 22:1 (erucic acid); modify wax composition or content, such as by altering the levels of C29, C31, or C33 alkanes; modify sterol composition or content, such as by altering the levels of brassicasterol, campesterol, stigmasterol, sitosterol or stigmastanol or the like, or modify glucosinolate composition or content.

Other seed characteristics that may be modified include traits relating to a seed's germination characteristics; shelf-life; drydown characteristics; size; stress responses, such as to heat, cold, salt or osmotic shock; other nutritional content, such as vitamins, minerals, or flavonoids; seedling vigor; pest resistance, or seed coat quality, resistance to pathogens, germination rate, resistance to heavy metals and toxins. Yet another desirable phenotype is a change in the overall gene expression pattern of the seed.

The polynucleotides of the invention encode plant transcription factors. The plant transcription factors are derived, e.g., from *Arabidopsis thaliana* and can belong, e.g., to one or more of the following transcription factor families: the AP2 (APETALA2) domain transcription factor family (Riechmann and Meyerowitz (1998) J. Biol. Chem. 379:633-646); the MYB transcription factor family (Martin and Paz-Ares (1997) Trends Genet. 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) J. Biol. Chem. 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) Mol. Gen. Genet. 244:563-571); the ankyrin-repeat protein family (Zhang et al. (1992) Plant Cell 4:1575-1588); the miscellaneous protein (MISC) family (Kim et al. (1997) Plant J. 11:1237-1251); the zinc finger protein (Z) family (Klug and Schwabe (1995) FASEB J. *9:* 597-604); the homeobox (HB) protein family (Duboule (1994) Guidebook to the Homeobox Genes, Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) Genes Dev. 3:1166-1178); the squamosa promoter binding proteins (SPB) (Klein et al. (1996) Mol. Gen. Genet. 1996 250:7-16); the NAM protein family; the IAA/AUX proteins (Rouse et al. (1998) Science 279:1371–1373); the HLH/MYC protein family (Littlewood et al. (1994) Prot. Profile 1:639-709); the DNA-binding protein (DBP) family (Tucker et al. (1994) EMBO J. 13:2994-3002); the bZIP family of transcription factors (Foster et al. (1994) FASEB J. 8:192-200); the BPF-1 protein (Box P-binding factor) family (da Costa e Silva et al. (1993) Plant J. 4:125-135); and the golden protein (GLD) family (Hall et al. (1998) Plant Cell 10:925-936).

In addition to methods for modifying a plant phenotype by employing one or more polynucleotides and polypeptides of the invention described herein, the polynucleotides and polypeptides of the invention have a variety of additional uses. These uses include their use in the recombinant production (i.e, expression) of proteins; as regulators of plant gene expression,

as diagnostic probes for the presence of complementary or partially complementary nucleic acids (including for detection of natural coding nucleic acids); as substrates for further reactions, e.g., mutation reactions, PCR reactions, or the like, of as substrates for cloning e.g., including digestion or ligation reactions, and for identifying exogenous or endogenous modulators of the transcription factors.

DEFINITIONS

A "polynucleotide" is a nucleic acid sequence comprising a plurality of polymerized nucleotide residues, e.g., at least about 15 consecutive polymerized nucleotide residues, optionally at least about 30 consecutive nucleotides, at least about 50 consecutive nucleotides. In many instances, a polynucleotide comprises a nucleotide sequence encoding a polypeptide (or protein) or a domain or fragment thereof. Additionally, the polynucleotide may comprise a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5' or 3' untranslated regions, a reporter gene, a selectable marker, or the like. The polynucleotide can be single stranded or double stranded DNA or RNA. The polynucleotide optionally comprises modified bases or a modified backbone. The polynucleotide can be, e.g., genomic DNA or RNA, a transcript (such as an mRNA), a cDNA, a PCR product, a cloned DNA, a synthetic DNA or RNA, or the like. The polynucleotide can comprise a sequence in either sense or antisense orientations.

A "recombinant polynucleotide" is a polynucleotide that is not in its native state, e.g., the polynucleotide comprises a nucleotide sequence not found in nature, or the polynucleotide is in a context other than that in which it is naturally found, e.g., separated from nucleotide sequences with which it typically is in proximity in nature, or adjacent (or contiguous with) nucleotide sequences with which it typically is not in proximity. For example, the sequence at issue can be cloned into a vector, or otherwise recombined with one or more additional nucleic acid.

An "isolated polynucleotide" is a polynucleotide whether naturally occurring or recombinant, that is present outside the cell in which it is typically found in nature, whether purified or not. Optionally, an isolated polynucleotide is subject to one or more enrichment or purification procedures, e.g., cell lysis, extraction, centrifugation, precipitation, or the like.

A "recombinant polypeptide" is a polypeptide produced by translation of a recombinant polynucleotide. An "isolated polypeptide," whether a naturally occurring or a recombinant polypeptide, is more enriched in (or out of) a cell than the polypeptide in its natural state in a wild type cell, e.g., more than about 5% enriched, more than about 10% enriched, or

more than about 20%, or more than about 50%, or more, enriched, i.e., alternatively denoted: 105%, 110%, 120%, 150% or more, enriched relative to wild type standardized at 100%. Such an enrichment is not the result of a natural response of a wild type plant. Alternatively, or additionally, the isolated polypeptide is separated from other cellular components with which it is typically associated, e.g., by any of the various protein purification methods herein.

The term "transgenic plant" refers to a plant that contains genetic material, not found in a wild type plant of the same species, variety or cultivar. The genetic material may include a transgene, an insertional mutagenesis event (such as by transposon or T-DNA insertional mutagenesis), an activation tagging sequence, a mutated sequence, a homologous recombination event or a sequence modified by chimeraplasty. Typically, the foreign genetic material has been introduced into the plant by human manipulation.

A transgenic plant may contain an expression vector or cassette. The expression cassette typically comprises a polypeptide-encoding sequence operably linked (i.e., under regulatory control of) to appropriate inducible or constitutive regulatory sequences that allow for the expression of polypeptide. The expression cassette can be introduced into a plant by transformation or by breeding after transformation of a parent plant. A plant refers to a whole plant as well as to a plant part, such as seed, fruit, leaf, or root, plant tissue, plant cells or any other plant material, e.g., a plant explant, as well as to progeny thereof, and to *in vitro* systems that mimic biochemical or cellular components or processes in a cell.

The phrase "ectopically expression or altered expression" in reference to a polynucleotide indicates that the pattern of expression in, e.g., a transgenic plant or plant tissue, is different from the expression pattern in a wild type plant or a reference plant of the same species. For example, the polynucleotide or polypeptide is expressed in a cell or tissue type other than a cell or tissue type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to altered expression patterns that are produced by lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern can be transient or stable, constitutive or inducible. In reference to a polypeptide, the term "ectopic expression or altered expression" further may relate to altered activity levels resulting from the interactions of the polypeptides with exogenous or endogenous modulators or from interactions with factors or as a result of the chemical modification of the polypeptides.

The term "fragment" or "domain," with respect to a polypeptide, refers to a subsequence of the polypeptide. In some cases, the fragment or domain, is a subsequence of the polypeptide which performs at least one biological function of the intact polypeptide in substantially the same manner, or to a similar extent, as does the intact polypeptide. For example, a polypeptide fragment can comprise a recognizable structural motif or functional domain such as a DNA binding domain that binds to a DNA promoter region, an activation domain or a domain for protein-protein interactions. Fragments can vary in size from as few as 6 amino acids to the full length of the intact polypeptide, but are preferably at least about 30 amino acids in length and more preferably at least about 60 amino acids in length. In reference to a nucleotide sequence, "a fragment" refers to any subsequence of a polynucleotide, typically, of at least consecutive about 15 nucleotides, preferably at least about 30 nucleotides, more preferably at least about 50, of any of the sequences provided herein.

The term "trait" refers to a physiological, morphological, biochemical or physical characteristic of a plant or particular plant material or cell. In some instances, this characteristic is visible to the human eye, such as seed or plant size, or can be measured by available biochemical techniques, such as the protein, starch or oil content of seed or leaves or by the observation of the expression level of genes, e.g., by employing Northern analysis, RT-PCR, microarray gene expression assays or reporter gene expression systems, or by agricultural observations such as stress tolerance, yield or pathogen tolerance.

"Trait modification" refers to a detectable difference in a characteristic in a plant ectopically expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. In some cases, the trait modification can be evaluated quantitatively. For example, the trait modification can entail at least about a 2% increase or decrease in an observed trait (difference), at least a 5% difference, at least about a 10% difference, at least about a 20% difference, at least about a 30%, at least about a 50%, at least about a 70%, or at least about a 100%, or an even greater difference. It is known that there can be a natural variation in the modified trait. Therefore, the trait modification observed entails a change of the normal distribution of the trait in the plants compared with the distribution observed in wild type plant.

Trait modifications of particular interest include those to seed (such as embryo or endosperm), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought, water saturation, radiation and ozone; improved tolerance to microbial, fungal or viral diseases; improved tolerance to pest infestations, including nematodes, mollicutes, parasitic higher plants or the like;

decreased herbicide sensitivity; improved tolerance of heavy metals or enhanced ability to take up heavy metals; improved growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotype that can be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenyllipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition. Physical plant characteristics that can be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves and roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that can be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, biomass or transpiration characteristics, as well as plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

POLYPEPTIDES AND POLYNUCLEOTIDES OF THE INVENTION

The present invention provides, among other things, transcription factors (TFs), and transcription factor homologue polypeptides, and isolated or recombinant polynucleotides encoding the polypeptides. These polypeptides and polynucleotides may be employed to modify a plant's seed characteristics.

Exemplary polynucleotides encoding the polypeptides of the invention were identified in the *Arabidopsis thaliana* GenBank database using publicly available sequence analysis programs and parameters. Sequences initially identified were then further characterized to identify sequences comprising specified sequence strings corresponding to sequence motifs present in families of known transcription factors. Polynucleotide sequences meeting such criteria were confirmed as transcription factors.

Additional polynucleotides of the invention were identified by screening *Arabidopsis thaliana* and/or other plant cDNA libraries with probes corresponding to known transcription factors under low stringency hybridization conditions. Additional sequences, including full length coding sequences were subsequently recovered by the rapid amplification of cDNA ends (RACE) procedure, using a commercially available kit according to the

manufacturer's instructions. Where necessary, multiple rounds of RACE are performed to isolate 5' and 3' ends. The full length cDNA was then recovered by a routine end-to-end polymerase chain reaction (PCR) using primers specific to the isolated 5' and 3' ends. Exemplary sequences are provided in the Sequence Listing.

The polynucleotides of the invention were ectopically expressed in overexpressor or knockout plants and changes in the seed characteristics of the plants were observed. Therefore, the polynucleotides and polypeptides can be employed to improve the seed characteristics of plants.

Making polynucleotides

The polynucleotides of the invention include sequences that encode transcription factors and transcription factor homologue polypeptides and sequences complementary thereto, as well as unique fragments of coding sequence, or sequence complementary thereto. Such polynucleotides can be, e.g., DNA or RNA, e.g., mRNA, cRNA, synthetic RNA, genomic DNA, cDNA synthetic DNA, oligonucleotides, etc. The polynucleotides are either double-stranded or single-stranded, and include either, or both sense (i.e., coding) sequences and antisense (i.e., non-coding, complementary) sequences. The polynucleotides include the coding sequence of a transcription factor, or transcription factor homologue polypeptide, in isolation, in combination with additional coding sequences (e.g., a purification tag, a localization signal, as a fusion-protein, as a pre-protein, or the like), in combination with non-coding sequences (e.g., introns or inteins, regulatory elements such as promoters, enhancers, terminators, and the like), and/or in a vector or host environment in which the polynucleotide encoding a transcription factor or transcription factor homologue polypeptide is an endogenous or exogenous gene.

A variety of methods exist for producing the polynucleotides of the invention. Procedures for identifying and isolating DNA clones are well known to those of skill in the art, and are described in, e.g., Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 Academic Press, Inc., San Diego, CA ("Berger"); Sambrook et al., Molecular Cloning - A Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989 ("Sambrook") and Current Protocols in Molecular Biology, F.M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 2000) ("Ausubel").

Alternatively, polynucleotides of the invention, can be produced by a variety of in vitro amplification methods adapted to the present invention by appropriate selection of specific or degenerate primers. Examples of protocols sufficient to direct persons of skill through in vitro amplification methods, including the polymerase chain reaction (PCR) the ligase chain

reaction (LCR), Qbeta-replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA), e.g., for the production of the homologous nucleic acids of the invention are found in Berger, Sambrook, and Ausubel, as well as Mullis et al., (1987) PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, CA (1990) (Innis). Improved methods for cloning in vitro amplified nucleic acids are described in Wallace et al., U.S. Pat. No. 5,426,039. Improved methods for amplifying large nucleic acids by PCR are summarized in Cheng et al. (1994) Nature 369: 684-685 and the references cited therein, in which PCR amplicons of up to 40kb are generated. One of skill will appreciate that essentially any RNA can be converted into a double stranded DNA suitable for restriction digestion, PCR expansion and sequencing using reverse transcriptase and a polymerase. *See*, e.g., Ausubel, Sambrook and Berger, *all supra.*

Alternatively, polynucleotides and oligonucleotides of the invention can be assembled from fragments produced by solid-phase synthesis methods. Typically, fragments of up to approximately 100 bases are individually synthesized and then enzymatically or chemically ligated to produce a desired sequence, e.g., a polynucletotide encoding all or part of a transcription factor. For example, chemical synthesis using the phosphoramidite method is described, e.g., by Beaucage et al. (1981) Tetrahedron Letters 22:1859-69; and Matthes et al. (1984) EMBO J. 3:801-5. According to such methods, oligonucleotides are synthesized, purified, annealed to their complementary strand, ligated and then optionally cloned into suitable vectors. And if so desired, the polynucleotides and polypeptides of the invention can be custom ordered from any of a number of commercial suppliers.

HOMOLOGOUS SEQUENCES

Sequences homologous, i.e., that share significant sequence identity or similarity, to those provided in the Sequence Listing, derived from *Arabidopsis thaliana* or from other plants of choice are also an aspect of the invention. Homologous sequences can be derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn, potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype

can be changed include barley, rye, millet, sorghum, currant, avocado, citrus fruits such as oranges, lemons, grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, and sweet potato, and beans. The homologous sequences may also be derived from woody species, such pine, poplar and eucalyptus.

Transcription factors that are homologous to the listed sequences will typically share at least about 31% amino acid sequence identity. More closely related transcription factors can share at least about 50%, about 60%, about 65%, about 70%, about 75% or about 80% or about 90% or about 95% or about 98% or more sequence identity with the listed sequences. Factors that are most closely related to the listed sequences share, e.g., at least about 85%, about 90% or about 95% or more % sequence identity to the listed sequences. At the nucleotide level, the sequences will typically share at least about 40% nucleotide sequence identity, preferably at least about 50%, about 60%, about 70% or about 80% sequence identity, and more preferably about 85%, about 90%, about 95% or about 97% or more sequence identity to one or more of the listed sequences. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein. Conserved domains within a transcription factor family may exhibit a higher degree of sequence homology, such as at least 65% sequence identity including conservative substitutions, and preferably at least 80% sequence identity.

Identifying Nucleic Acids by Hybridization

Polynucleotides homologous to the sequences illustrated in the Sequence Listing can be identified, e.g., by hybridization to each other under stringent or under highly stringent conditions. Single stranded polynucleotides hybridize when they associate based on a variety of well characterized physico-chemical forces, such as hydrogen bonding, solvent exclusion, base stacking and the like. The stringency of a hybridization reflects the degree of sequence identity of the nucleic acids involved, such that the higher the stringency, the more similar are the two polynucleotide strands. Stringency is influenced by a variety of factors, including temperature, salt concentration and composition, organic and non-organic additives, solvents, etc. present in both the hybridization and wash solutions and incubations (and number), as described in more detail in the references cited above.

An example of stringent hybridization conditions for hybridization of complementary nucleic acids which have more than 100 complementary residues on a filter in a Southern or northern blot is about 5°C to 20°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined

ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions, e.g., to a unique subsequence, of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C, for example 0.2 x SSC, 0.1% SDS at 65° C. For identification of less closely related homologues washes can be performed at a lower temperature, e.g., 50° C. In general, stringency is increased by raising the wash temperature and/or decreasing the concentration of SSC.

As another example, stringent conditions can be selected such that an oligonucleotide that is perfectly complementary to the coding oligonucleotide hybridizes to the coding oligonucleotide with at least about a 5-10x higher signal to noise ratio than the ratio for hybridization of the perfectly complementary oligonucleotide to a nucleic acid encoding a transcription factor known as of the filing date of the application. Conditions can be selected such that a higher signal to noise ratio is observed in the particular assay which is used, e.g., about 15x, 25x, 35x, 50x or more. Accordingly, the subject nucleic acid hybridizes to the unique coding oligonucleotide with at least a 2x higher signal to noise ratio as compared to hybridization of the coding oligonucleotide to a nucleic acid encoding known polypeptide. Again, higher signal to noise ratios can be selected, e.g., about 5x, 10x, 25x, 35x, 50x or more. The particular signal will depend on the label used in the relevant assay, e.g., a fluorescent label, a colorimetric label, a radio active label, or the like.

Alternatively, transcription factor homologue polypeptides can be obtained by screening an expression library using antibodies specific for one or more transcription factors. With the provision herein of the disclosed transcription factor, and transcription factor homologue nucleic acid sequences, the encoded polypeptide(s) can be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or polyclonal) specific for the polypeptide(s) in question. Antibodies can also be raised against synthetic peptides derived from transcription factor, or transcription factor homologue, amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression library produced from the plant from which it is desired to clone additional transcription factor homologues, using the methods described above. The selected cDNAs can be confirmed by sequencing and enzymatic activity.

SEQUENCE VARIATIONS

It will readily be appreciated by those of skill in the art, that any of a variety of polynucleotide sequences are capable of encoding the transcription factors and transcription factor homologue polypeptides of the invention. Due to the degeneracy of the genetic code, many different polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing.

For example, Table 1 illustrates, e.g., that the codons AGC, AGT, TCA, TCC, TCG, and TCT all encode the same amino acid: serine. Accordingly, at each position in the sequence where there is a codon encoding serine, any of the above trinucleotide sequences can be used without altering the encoded polypeptide.

Table 1

Amino acids			Codon					
Alanine	Ala	A	GCA	GCC	GCG	GCU		
Cysteine	Cys	C	TGC	TGT				
Aspartic acid	Asp	D	GAC	GAT				
Glutamic acid	Glu	E	GAA	GAG				
Phenylalanine	Phe	F	TTC	TTT				
Glycine	Gly	G	GGA	GGC	GGG	GGT		
Histidine	His	H	CAC	CAT				
Isoleucine	Ile	I	ATA	ATC	ATT			
Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	TTA	TTG	CTA	CTC	CTG	CTT
Methionine	Met	M	ATG					
Asparagine	Asn	N	AAC	AAT				
Proline	Pro	P	CCA	CCC	CCG	CCT		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGT
Serine	Ser	S	AGC	AGT	TCA	TCC	TCG	TCT
Threonine	Thr	T	ACA	ACC	ACG	ACT		
Valine	Val	V	GTA	GTC	GTG	GTT		
Tryptophan	Trp	W	TGG					
Tyrosine	Tyr	Y	TAC	TAT				

Sequence alterations that do not change the amino acid sequence encoded by the polynucleotide are termed "silent" variations. With the exception of the codons ATG and TGG, encoding methionine and tryptophan, respectively, any of the possible codons for the same amino acid can be substituted by a variety of techniques, e.g., site-directed mutagenesis, available in the art. Accordingly, any and all such variations of a sequence selected from the above table are a feature of the invention.

In addition to silent variations, other conservative variations that alter one, or a few amino acids in the encoded polypeptide, can be made without altering the function of the polypeptide, these conservative variants are, likewise, a feature of the invention.

For example, substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) Meth. Enzymol. (1993) vol. 217, Academic Press) or the other methods noted below. Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof can be combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure. Preferably, the polypeptide encoded by the DNA performs the desired function.

Conservative substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the Table 2 when it is desired to maintain the activity of the protein. Table 2 shows amino acids which can be substituted for an amino acid in a protein and which are typically regarded as conservative substitutions.

Table 2

Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Gln	Asn
Cys	Ser
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr; Gly
Thr	Ser;Val
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Substitutions that are less conservative than those in Table 2 can be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

FURTHER MODIFYING SEQUENCES OF THE INVENTION—MUTATION/ FORCED EVOLUTION

In addition to generating silent or conservative substitutions as noted, above, the present invention optionally includes methods of modifying the sequences of the Sequence Listing. In the methods, nucleic acid or protein modification methods are used to alter the given sequences to produce new sequences and/or to chemically or enzymatically modify given sequences to change the properties of the nucleic acids or proteins.

Thus, in one embodiment, given nucleic acid sequences are modified, e.g., according to standard mutagenesis or artificial evolution methods to produce modified sequences. For example, Ausubel, *supra*, provides additional details on mutagenesis methods. Artificial forced evolution methods are described, e.g., by Stemmer (1994) Nature 370:389-391, and Stemmer (1994) Proc. Natl. Acad. Sci. USA 91:10747-10751. Many other mutation and evolution methods are also available and expected to be within the skill of the practitioner.

Similarly, chemical or enzymatic alteration of expressed nucleic acids and polypeptides can be performed by standard methods. For example, sequence can be modified by addition of lipids, sugars, peptides, organic or inorganic compounds, by the inclusion of modified nucleotides or amino acids, or the like. For example, protein modification techniques are illustrated in Ausubel, *supra*. Further details on chemical and enzymatic modifications can be found herein. These modification methods can be used to modify any given sequence, or to modify any sequence produced by the various mutation and artificial evolution modification methods noted herein.

Accordingly, the invention provides for modification of any given nucleic acid by mutation, evolution, chemical or enzymatic modification, or other available methods, as well as for the products produced by practicing such methods, e.g., using the sequences herein as a starting substrate for the various modification approaches.

For example, optimized coding sequence containing codons preferred by a particular prokaryotic or eukaryotic host can be used e.g., to increase the rate of translation or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, as compared with transcripts produced using a non-optimized sequence. Translation stop codons can also be modified to reflect host preference. For example, preferred stop codons for *S. cerevisiae* and mammals are TAA and TGA, respectively. The preferred stop codon for monocotyledonous plants is TGA, whereas insects and *E. coli* prefer to use TAA as the stop codon.

The polynucleotide sequences of the present invention can also be engineered in order to alter a coding sequence for a variety of reasons, including but not limited to, alterations which modify the sequence to facilitate cloning, processing and/or expression of the gene product. For example, alterations are optionally introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, to introduce splice sites, etc.

Furthermore, a fragment or domain derived from any of the polypeptides of the invention can be combined with domains derived from other transcription factors or synthetic domains to modify the biological activity of a transcription factor. For instance, a DNA binding domain derived from a transcription factor of the invention can be combined with the activation domain of another transcription factor or with a synthetic activation domain. A transcription activation domain assists in initiating transcription from a DNA binding site. Examples include the transcription activation region of VP16 or GAL4 (Moore et al. (1998) Proc. Natl. Acad. Sci. USA 95: 376-381; and Aoyama et al. (1995) Plant Cell 7:1773-1785), peptides derived from bacterial sequences (Ma and Ptashne (1987) Cell 51; 113-119) and synthetic peptides (Giniger and Ptashne, (1987) Nature 330:670-672).

EXPRESSION AND MODIFICATION OF POLYPEPTIDES

Typically, polynucleotide sequences of the invention are incorporated into recombinant DNA (or RNA) molecules that direct expression of polypeptides of the invention in appropriate host cells, transgenic plants, in vitro translation systems, or the like. Due to the inherent degeneracy of the genetic code, nucleic acid sequences which encode substantially the same or a functionally equivalent amino acid sequence can be substituted for any listed sequence to provide for cloning and expressing the relevant homologue.

Vectors, Promoters and Expression Systems

The present invention includes recombinant constructs comprising one or more of the nucleic acid sequences herein. The constructs typically comprise a vector, such as a plasmid, a cosmid, a phage, a virus (e.g., a plant virus), a bacterial artificial chromosome (BAC), a yeast artificial chromosome (YAC), or the like, into which a nucleic acid sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available.

General texts which describe molecular biological techniques useful herein, including the use and production of vectors, promoters and many other relevant topics, include Berger, Sambrook and Ausubel, *supra*. Any of the identified sequences can be incorporated into a cassette or vector, e.g., for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in Weissbach and Weissbach, (1989) Methods for Plant Molecular Biology, Academic Press, and Gelvin et al., (1990) Plant Molecular Biology Manual, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella et al. (1983) Nature 303: 209, Bevan (1984) Nucl Acid Res. 12: 8711-8721, Klee (1985) Bio/Technology 3: 637-642, for dicotyledonous plants.

Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods can involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou (1991) Bio/Technology 9: 957-962) and corn (Gordon-Kamm (1990) Plant Cell 2: 603-618) can be produced. An immature embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks et al. (1993) Plant Physiol 102: 1077-1084; Vasil (1993) Bio/Technology 10: 667-674; Wan and Lemeaux (1994) Plant Physiol 104: 37-48, and for Agrobacterium-mediated DNA transfer (Ishida et al. (1996) Nature Biotech 14: 745-750).

Typically, plant transformation vectors include one or more cloned plant coding sequence (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

Examples of constitutive plant promoters which can be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (*see*, e.g., Odel et al. (1985) Nature 313:810); the nopaline synthase promoter (An et al. (1988) Plant Physiol 88:547); and the octopine synthase promoter (Fromm et al. (1989) Plant Cell 1: 977).

A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of a TF sequence in plants. Choice of a promoter is based largely on the phenotype of interest and is determined by such factors as tissue (e.g., seed, fruit, root, pollen, vascular tissue, flower, carpel, etc.), inducibility (e.g., in response to wounding, heat, cold, drought, light, pathogens, etc.), timing, developmental stage, and the like. Numerous known promoters have been characterized and can favorable be employed to promote expression of a polynucleotide of the invention in a transgenic plant or cell of interest. For example, tissue specific promoters include: seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No. 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) Plant Mol Biol 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) Plant Mol Biol 37:977-988), flower-specific (Kaiser et al, (1995) Plant Mol Biol 28:231-243), pollen (Baerson et al. (1994) Plant Mol Biol 26:1947-1959), carpels (Ohl et al. (1990) Plant Cell 2:837-848), pollen and ovules (Baerson et al. (1993) Plant Mol Biol 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al. (1999) Plant Mol Biol 39:979-990 or Baumann et al. (1999) Plant Cell 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) Plant Mol Biol 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) Plant Mol Biol 38:1053-1060, Willmott et al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley et al. (1993) Plant Mol Biol 22: 13-23), light (e.g., the pea rbcS-3A promoter, Kuhlemeier et al. (1989) Plant Cell 1:471, and the maize rbcS promoter, Schaffner and Sheen (1991) Plant Cell 3: 997); wounding (e.g., *wunI*, Siebertz et al. (1989) Plant Cell 1: 961); pathogens (such as the PR-1 promoter described in Buchel et al. (1999) Plant Mol. Biol. 40:387-396, and the PDF1.2 promoter described in Manners et al. (1998) Plant Mol. Biol. 38:1071-80), and chemicals such as methyl jasmonate or salicylic acid (Gatz et al. (1997) Plant Mol Biol 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (An and Amazon (1995) Science 270: 1986-1988); or late seed development (Odell et al. (1994) Plant Physiol 106:447-458).

Plant expression vectors can also include RNA processing signals that can be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors can include additional regulatory sequences from the 3'-untranslated region of plant

genes, e.g., a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Additional Expression Elements

Specific initiation signals can aid in efficient translation of coding sequences. These signals can include, e.g., the ATG initiation codon and adjacent sequences. In cases where a coding sequence, its initiation codon and upstream sequences are inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only coding sequence (e.g., a mature protein coding sequence), or a portion thereof, is inserted, exogenous transcriptional control signals including the ATG initiation codon can be separately provided. The initiation codon is provided in the correct reading frame to facilitate transcription. Exogenous transcriptional elements and initiation codons can be of various origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of enhancers appropriate to the cell system in use.

Expression Hosts

The present invention also relates to host cells which are transduced with vectors of the invention, and the production of polypeptides of the invention (including fragments thereof) by recombinant techniques. Host cells are genetically engineered (i.e, nucleic acids are introduced, e.g., transduced, transformed or transfected) with the vectors of this invention, which may be, for example, a cloning vector or an expression vector comprising the relevant nucleic acids herein. The vector is optionally a plasmid, a viral particle, a phage, a naked nucleic acids, *etc.* The engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants, or amplifying the relevant gene. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to those skilled in the art and in the references cited herein, including, Sambrook and Ausubel.

The host cell can be a eukaryotic cell, such as a yeast cell, or a plant cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Plant protoplasts are also suitable for some applications. For example, the DNA fragments are introduced into plant tissues, cultured plant cells or plant protoplasts by standard methods including electroporation (Fromm et al., (1985) Proc. Natl. Acad. Sci. USA 82, 5824, infection by viral vectors such as cauliflower mosaic virus (CaMV) (Hohn et al., (1982) Molecular Biology of Plant Tumors, (Academic Press, New York) pp. 549-560; US 4,407,956), high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., (1987) Nature 327, 70-73), use of pollen as vector (WO 85/01856), or use of *Agrobacterium*

tumefaciens or *A. rhizogenes* carrying a T-DNA plasmid in which DNA fragments are cloned. The T-DNA plasmid is transmitted to plant cells upon infection by *Agrobacterium tumefaciens*, and a portion is stably integrated into the plant genome (Horsch et al. (1984) Science 233:496-498; Fraley et al. (1983) Proc. Natl. Acad. Sci. USA 80, 4803).

The cell can include a nucleic acid of the invention which encodes a polypeptide, wherein the cells expresses a polypeptide of the invention. The cell can also include vector sequences, or the like. Furthermore, cells and transgenic plants which include any polypeptide or nucleic acid above or throughout this specification, e.g., produced by transduction of a vector of the invention, are an additional feature of the invention.

For long-term, high-yield production of recombinant proteins, stable expression can be used. Host cells transformed with a nucleotide sequence encoding a polypeptide of the invention are optionally cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The protein or fragment thereof produced by a recombinant cell may be secreted, membrane-bound, or contained intracellularly, depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides encoding mature proteins of the invention can be designed with signal sequences which direct secretion of the mature polypeptides through a prokaryotic or eukaryotic cell membrane.

Modified Amino Acids

Polypeptides of the invention may contain one or more modified amino acids. The presence of modified amino acids may be advantageous in, for example, increasing polypeptide half-life, reducing polypeptide antigenicity or toxicity, increasing polypeptide storage stability, or the like. Amino acid(s) are modified, for example, co-translationally or post-translationally during recombinant production or modified by synthetic or chemical means.

Non-limiting examples of a modified amino acid include incorporation or other use of acetylated amino acids, glycosylated amino acids, sulfated amino acids, prenylated (e.g., farnesylated, geranylgeranylated) amino acids, PEG modified (e.g., "PEGylated") amino acids, biotinylated amino acids, carboxylated amino acids, phosphorylated amino acids, etc. References adequate to guide one of skill in the modification of amino acids are replete throughout the literature.

IDENTIFICATION OF ADDITIONAL FACTORS

A transcription factor provided by the present invention can also be used to identify additional endogenous or exogenous molecules that can affect a phentoype or trait of

interest. On the one hand, such molecules include organic (small or large molecules) and/or inorganic compounds that affect expression of (i.e., regulate) a particular transcription factor. Alternatively, such molecules include endogenous molecules that are acted upon either at a transcriptional level by a transcription factor of the invention to modify a phenotype as desired. For example, the transcription factors can be employed to identify one or more downstream gene with which is subject to a regulatory effect of the transcription factor. In one approach, a transcription factor or transcription factor homologue of the invention is expressed in a host cell, e.g, a transgenic plant cell, tissue or explant, and expression products, either RNA or protein, of likely or random targets are monitored, e.g., by hybridization to a microarray of nucleic acid probes corresponding to genes expressed in a tissue or cell type of interest, by two-dimensional gel electrophoresis of protein products, or by any other method known in the art for assessing expression of gene products at the level of RNA or protein. Alternatively, a transcription factor of the invention can be used to identify promoter sequences (i.e., binding sites) involved in the regulation of a downstream target. After identifying a promoter sequence, interactions between the transcription factor and the promoter sequence can be modified by changing specific nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences can be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the transcription factors with their promoters (Bulyk et al. (1999) Nature Biotechnology 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification can occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or-heteropolymer) interactions. Any method suitable for detecting protein-protein interactions can be employed. Among the methods that can be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in Chien, et al., (1991), Proc. Natl. Acad. Sci. USA 88, 9578-9582 and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid

and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions can be preformed.

IDENTIFICATION OF MODULATORS

In addition to the intracellular molecules described above, extracellular molecules that alter activity or expression of a transcription factor, either directly or indirectly, can be identified. For example, the methods can entail first placing a candidate molecule in contact with a plant or plant cell. The molecule can be introduced by topical administration, such as spraying or soaking of a plant, and then the molecule's effect on the expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide can be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence can be detected by use of microarrays, Northems, quantitative PCR, or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds) Current Protocols in Molecular Biology, John Wiley & Sons (1998). Such changes in the expression levels can be correlated with modified plant traits and thus identified molecules can be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

Essentially any available composition can be tested for modulatory activity of expression or activity of any nucleic acid or polypeptide herein. Thus, available libraries of compounds such as chemicals, polypeptides, nucleic acids and the like can be tested for modulatory activity. Often, potential modulator compounds can be dissolved in aqueous or organic (e.g., DMSO-based) solutions for easy delivery to the cell or plant of interest in which the activity of the modulator is to be tested. Optionally, the assays are designed to screen large modulator composition libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays).

In one embodiment, high throughput screening methods involve providing a combinatorial library containing a large number of potential compounds (potential modulator compounds). Such "combinatorial chemical libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as target compounds.

A combinatorial chemical library can be, e.g., a collection of diverse chemical compounds generated by chemical synthesis or biological synthesis. For example, a combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (e.g., in one example, amino acids) in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound of a set length). Exemplary libraries include peptide libraries, nucleic acid libraries, antibody libraries (see, e.g., Vaughn et al. (1996) Nature Biotechnology, 14(3):309-314 and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al. Science (1996) 274:1520-1522 and U.S. Patent 5,593,853), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), and small organic molecule libraries (see, e.g., benzodiazepines, Baum C&EN Jan 18, page 33 (1993); isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337) and the like.

Preparation and screening of combinatorial or other libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent 5,010,175, Furka, Int. J. Pept. Prot. Res. 37:487-493 (1991) and Houghton et al. Nature 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used.

In addition, as noted, compound screening equipment for high-throughput screening is generally available, e.g., using any of a number of well known robotic systems that have also been developed for solution phase chemistries useful in assay systems. These systems include automated workstations including an automated synthesis apparatus and robotic systems utilizing robotic arms. Any of the above devices are suitable for use with the present invention, e.g., for high-throughput screening of potential modulators. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art.

Indeed, entire high throughput screening systems are commercially available. These systems typically automate entire procedures including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s)

appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. Similarly, microfluidic implementations of screening are also commercially available.

The manufacturers of such systems provide detailed protocols the various high throughput. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like. The integrated systems herein, in addition to providing for sequence alignment and, optionally, synthesis of relevant nucleic acids, can include such screening apparatus to identify modulators that have an effect on one or more polynucleotides or polypeptides according to the present invention.

In some assays it is desirable to have positive controls to ensure that the components of the assays are working properly. At least two types of positive controls are appropriate. That is, known transcriptional activators or inhibitors can be incubated with cells/plants/ etc. in one sample of the assay, and the resulting increase/decrease in transcription can be detected by measuring the resulting increase in RNA/ protein expression, etc., according to the methods herein. It will be appreciated that modulators can also be combined with transcriptional activators or inhibitors to find modulators which inhibit transcriptional activation or transcriptional repression. Either expression of the nucleic acids and proteins herein or any additional nucleic acids or proteins activated by the nucleic acids or proteins herein, or both, can be monitored.

In an embodiment, the invention provides a method for identifying compositions that modulate the activity or expression of a polynucleotide or polypeptide of the invention. For example, a test compound, whether a small or large molecule, is placed in contact with a cell, plant (or plant tissue or explant), or composition comprising the polynucleotide or polypeptide of interest and a resulting effect on the cell, plant, (or tissue or explant) or composition is evaluated by monitoring, either directly or indirectly, one or more of: expression level of the polynucleotide or polypeptide, activity (or modulation of the activity) of the polynucleotide or polypeptide. In some cases, an alteration in a plant phenotype can be detected following contact of a plant (or plant cell, or tissue or explant) with the putative modulator, e.g., by modulation of expression or activity of a polynucleotide or polypeptide of the invention.

SUBSEQUENCES

Also contemplated are uses of polynucleotides, also referred to herein as oligonucleotides, typically having at least 12 bases, preferably at least 15, more preferably at least

20, 30, or 50 bases, which hybridize under at least highly stringent (or ultra-high stringent or ultra-ultra- high stringent conditions) conditions to a polynucleotide sequence described above. The polynucleotides may be used as probes, primers, sense and antisense agents, and the like, according to methods as noted *supra*.

Subsequences of the polynucleotides of the invention, including polynucleotide fragments and oligonucleotides are useful as nucleic acid probes and primers. An oligonucleotide suitable for use as a probe or primer is at least about 15 nucleotides in length, more often at least about 18 nucleotides, often at least about 21 nucleotides, frequently at least about 30 nucleotides, or about 40 nucleotides, or more in length. A nucleic acid probe is useful in hybridization protocols, e.g., to identify additional polypeptide homologues of the invention, including protocols for microarray experiments. Primers can be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook and Ausubel, *supra*.

In addition, the invention includes an isolated or recombinant polypeptide including a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotides of the invention. For example, such polypeptides, or domains or fragments thereof, can be used as immunogens, e.g., to produce antibodies specific for the polypeptide sequence, or as probes for detecting a sequence of interest. A subsequence can range in size from about 15 amino acids in length up to and including the full length of the polypeptide.

PRODUCTION OF TRANSGENIC PLANTS

Modification of Traits

The polynucleotides of the invention are favorably employed to produce transgenic plants with various traits, or characteristics, that have been modified in a desirable manner, e.g., to improve the seed characteristics of a plant. For example, alteration of expression levels or patterns (e.g., spatial or temporal expression patterns) of one or more of the transcription factors (or transcription factor homologues) of the invention, as compared with the levels of the same protein found in a wild type plant, can be used to modify a plant's traits. An illustrative example of trait modification, improved seed characteristics, by altering expression levels of a particular transcription factor is described further in the Examples and the Sequence Listing.

Antisense and Cosuppression Approaches

In addition to expression of the nucleic acids of the invention as gene replacement or plant phenotype modification nucleic acids, the nucleic acids are also useful for sense and anti-sense suppression of expression, e.g., to down-regulate expression of a nucleic acid of the invention, e.g., as a further mechanism for modulating plant phenotype. That is, the nucleic acids of the invention, or subsequences or anti-sense sequences thereof, can be used to block expression of naturally occurring homologous nucleic acids. A variety of sense and anti-sense technologies are known in the art, e.g., as set forth in Lichtenstein and Nellen (1997) Antisense Technology: A Practical Approach IRL Press at Oxford University, Oxford, England. In general, sense or anti-sense sequences are introduced into a cell, where they are optionally amplified, e.g., by transcription. Such sequences include both simple oligonucleotide sequences and catalytic sequences such as ribozymes.

For example, a reduction or elimination of expression (i.e., a "knock-out") of a transcription factor or transcription factor homologue polypeptide in a transgenic plant, e.g., to modify a plant trait, can be obtained by introducing an antisense construct corresponding to the polypeptide of interest as a cDNA. For antisense suppression, the transcription factor or homologue cDNA is arranged in reverse orientation (with respect to the coding sequence) relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length cDNA or gene, and need not be identical to the cDNA or gene found in the plant type to be transformed. Typically, the antisense sequence need only be capable of hybridizing to the target gene or RNA of interest. Thus, where the introduced sequence is of shorter length, a higher degree of homology to the endogenous transcription factor sequence will be needed for effective antisense suppression. While antisense sequences of various lengths can be utilized, preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous transcription factor gene in the plant cell.

Suppression of endogenous transcription factor gene expression can also be achieved using a ribozyme. Ribozymes are RNA molecules that possess highly specific endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 and U.S. Patent No. 5,543,508. Synthetic ribozyme sequences including antisense RNAs can be used to confer RNA cleaving activity on the antisense RNA, such that endogenous

mRNA molecules that hybridize to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Vectors in which RNA encoded by a transcription factor or transcription factor homologue cDNA is over-expressed can also be used to obtain co-suppression of a corresponding endogenous gene, e.g., in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire transcription factor cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous transcription factor gene of interest. However, as with antisense suppression, the suppressive efficiency will be enhanced as specificity of hybridization is increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity between the introduced sequence and the endogenous transcription factor gene is increased.

Vectors expressing an untranslatable form of the transcription factor mRNA, e.g., sequences comprising one or more stop codon, or nonsense mutation) can also be used to suppress expression of an endogenous transcription factor, thereby reducing or eliminating it's activity and modifying one or more traits. Methods for producing such constructs are described in U.S. Patent No. 5,583,021. Preferably, such constructs are made by introducing a premature stop codon into the transcription factor gene. Alternatively, a plant trait can be modified by gene silencing using double-strand RNA (Sharp (1999) Genes and Development 13: 139-141).

Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a transcription factor or transcription factor homologue gene. Plants containing a single transgene insertion event at the desired gene can be crossed to generate homozygous plants for the mutation (Koncz et al. (1992) Methods in Arabidopsis Research, World Scientific).

Alternatively, a plant phenotype can be altered by eliminating an endogenous gene, such as a transcription factor or transcription factor homologue, e.g., by homologous recombination (Kempin et al. (1997) Nature 389:802).

A plant trait can also be modified by using the cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome can be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the intervening DNA sequence between the two sites is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention can also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of

the endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al. (1997) Nature 390 698-701; Kakimoto et al. (1996) Science 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery in a plant can be modified so as to increase transcription levels of a polynucleotide of the invention (*See*, e.g., PCT Publications WO 96/06166 and WO 98/53057 which describe the modification of the DNA binding specificity of zinc finger proteins by changing particular amino acids in the DNA binding motif).

The transgenic plant can also include the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state.

Transgenic plants (or plant cells, or plant explants, or plant tissues) incorporating the polynucleotides of the invention and/or expressing the polypeptides of the invention can be produced by a variety of well established techniques as described above. Following construction of a vector, most typically an expression cassette, including a polynucleotide, e.g., encoding a transcription factor or transcription factor homologue, of the invention, standard techniques can be used to introduce the polynucleotide into a plant, a plant cell, a plant explant or a plant tissue of interest. Optionally, the plant cell, explant or tissue can be regenerated to produce a transgenic plant.

The plant can be any higher plant, including gymnosperms, monocotyledonous and dicotyledenous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover, etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcurbitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) Handbook of Plant Cell Culture –Crop Species. Macmillan Publ. Co. Shimamoto et al. (1989) Nature 338:274-276; Fromm et al. (1990) Bio/Technology 8:833-839; and Vasil et al. (1990) Bio/Technology 8:429-434.

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable methods can include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated

transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumeficiens* mediated transformation. Transformation means introducing a nucleotide sequence in a plant in a manner to cause stable or transient expression of the sequence.

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait can be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention can be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

INTEGRATED SYSTEMS—SEQUENCE IDENTITY

Additionally, the present invention may be an integrated system, computer or computer readable medium that comprises an instruction set for determining the identity of one or more sequences in a database. In addition, the instruction set can be used to generate or identify sequences that meet any specified criteria. Furthermore, the instruction set may be used to associate or link certain functional benefits, such improved seed characteristics, with one or more identified sequence.

For example, the instruction set can include, e.g., a sequence comparison or other alignment program, e.g., an available program such as, for example, the Wisconsin Package Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madision, WI). Public sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PhytoSeq (Incyte Pharmaceuticals, Palo Alto, CA) can be searched.

Alignment of sequences for comparison can be conducted by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Natl. Acad. Sci. U.S.A. 85: 2444, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence similarity. The comparison window can be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al., *supra*.

A variety of methods of determining sequence relationships can be used, including manual alignment and computer assisted sequence alignment and analysis. This later approach is a preferred approach in the present invention, due to the increased throughput afforded by computer assisted methods. As noted above, a variety of computer programs for performing sequence alignment are available, or can be produced by one of skill.

One example algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al. J. Mol. Biol 215:403-410 (1990). Software for performing BLAST analyses is publicly available, e.g., through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an

expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, an expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915).

In addition to calculating percent sequence identity, the BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see*, e.g., Karlin & Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence (and, therefore, in this context, homologous) if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.1, or less than about 0.01, and or even less than about 0.001. An additional example of a useful sequence alignment algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. The program can align, e.g., up to 300 sequences of a maximum length of 5,000 letters.

The integrated system, or computer typically includes a user input interface allowing a user to selectively view one or more sequence records corresponding to the one or more character strings, as well as an instruction set which aligns the one or more character strings with each other or with an additional character string to identify one or more region of sequence similarity. The system may include a link of one or more character strings with a particular phenotype or gene function. Typically, the system includes a user readable output element which displays an alignment produced by the alignment instruction set.

The methods of this invention can be implemented in a localized or distributed computing environment. In a distributed environment, the methods may implemented on a single computer comprising multiple processors or on a multiplicity of computers. The computers can be linked, e.g. through a common bus, but more preferably the computer(s) are nodes on a network. The network can be a generalized or a dedicated local or wide-area network and, in certain preferred embodiments, the computers may be components of an intra-net or an internet.

Thus, the invention provides methods for identifying a sequence similar or homologous to one or more polynucleotides as noted herein, or one or more target polypeptides encoded by the polynucleotides, or otherwise noted herein and may include linking or associating a given plant phenotype or gene function with a sequence. In the methods, a sequence database is

provided (locally or across an inter or intra net) and a query is made against the sequence database using the relevant sequences herein and associated plant phenotypes or gene functions.

Any sequence herein can be entered into the database, before or after querying the database. This provides for both expansion of the database and, if done before the querying step, for insertion of control sequences into the database. The control sequences can be detected by the query to ensure the general integrity of both the database and the query. As noted, the query can be performed using a web browser based interface. For example, the database can be a centralized public database such as those noted herein, and the querying can be done from a remote terminal or computer across an internet or intranet.

EXAMPLES

The following examples are intended to illustrate but not limit the present invention.

EXAMPLE I. FULL LENGTH GENE IDENTIFICATION AND CLONING

Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of –4 or –5 or lower, depending on the length of the query sequence. Putative transcription factor sequence hits were then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

Alternatively, Arabidopsis *thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60° C) and labeled with ^{32}P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M $NaPO_4$ pH 7.0, 7% SDS, 1 % w/v bovine serum albumin) and hybridized overnight at 60 °C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSCC, 1% SDS at 60° C.

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the Marathon™ cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded

cDNA, blunting cDNA ends, followed by ligation of the Marathon™ Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA.

Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained, sequenced and cloned. The process can be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

EXAMPLE II. CONSTRUCTION OF EXPRESSION VECTORS

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN20 or pMEN65, which are both derived from pMON316 (Sanders et al, (1987) Nucleic Acids Research 15:1543-58) and contain the CaMV 35S promoter to express transgenes. To clone the sequence into the vector, both pMEN20 and the amplified DNA fragment were digested separately with SalI and NotI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, CA). The fragments of interest were ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma).

Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini Prep kits (Qiagen, CA).

EXAMPLE III. TRANSFORMATION OF *AGROBACTERIUM* WITH THE EXPRESSION VECTOR

After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. (1990) FEMS Microbiol Letts. 67: 325-328. *Agrobacterium* strain ABI was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance (A_{600}) of 0.5 – 1.0 was reached. Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were then

resuspended in 250 µl chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 µl chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 µl and 750 µl, respectively. Resuspended cells were then distributed into 40 µl aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

Agrobacterium cells were transformed with plasmids prepared as described above following the protocol described by Nagel et al. For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 µl of *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 µF and 200 µF using a Gene Pulser II apparatus (Bio-Rad). After electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100 µg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The presence of the plasmid construct was verified by PCR amplification and sequence analysis.

EXAMPLE IV. TRANSFORMATION OF *ARABIDOPSIS* PLANTS WITH A*GROBACTERIUM TUMEFACIENS* WITH EXPRESSION VECTOR

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an absorbance (A_{600}) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 µM benzylamino purine (Sigma), 200 µl/L Silwet L-77 (Lehle Seeds) until an absorbance (A_{600}) of 0.8 was reached.

Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium (Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under continuous illumination (50-75 $\mu E/m^2/sec$) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

EXAMPLE V. IDENTIFICATION OF ARABIDOPSIS PRIMARY TRANSFORMANTS

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H_2O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H_2O. The seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH), 1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under continuous illumination (50-75 $\mu E/m^2/sec$) at 22-23° C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T_1 generation) were visible and obtained. These seedlings were transferred first to fresh selection plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

Primary transformants were crossed and progeny seeds (T_2) collected; kanamycin resistant seedlings were selected and analyzed. The expression levels of the recombinant polynucleotides in the transformants varies from about a 5% expression level increase to a least a 100% expression level increase. Similar observations are made with respect to polypeptide level expression.

EXAMPLE VI. IDENTIFICATION OF ARABIDOPSIS PLANTS WITH TRANSCRIPTION FACTOR GENE KNOCKOUTS

The screening of insertion mutagenized *Arabidopsis* collections for null mutants in a known target gene was essentially as described in Krysan et al (1999) Plant Cell 11:2283-2290. Briefly, gene-specific primers, nested by 5-250 pb to each others, were designed from the 5' and 3' regions of a known target gene. Similarly, nested sets of primers were also created specific to each of the T-DNA or transposon ends (the "right" and "left" borders). All possible combinations of gene specific and T-DNA/transposon primers were used to detect by PCR an insertion event within or close to the target gene. The amplified DNA fragments were then sequenced which allows the precise determination of the T-DNA/transposon insertion point relative to the target gene. Insertion events within the coding or intervening sequence of the genes were deconvoluted from a pool comprising a plurality of insertion events to a single unique mutant plant for functional characterization. The method is described in more detail in Yu and Adam, US Application Serial No. 09/177,733 filed October 23, 1998.

EXAMPLE VII. IDENTIFICATION OF SEED CHARACTERISTICS PHENOTYPE IN OVEREXPRESSOR OR GENE KNOCKOUT PLANTS

Experiments were performed to identify those transformants or knockouts that exhibited an improved seed characteristics. For such studies, the transformants were observed by eye or biochemical assays were performed.

Among the biochemicals that were assayed were insoluble sugars, such as arabinose, fucose, galactose,.mannose, rhamnose or xylose or the like; prenyl lipids, such as lutein, beta-carotene, xanthophyll-1, xanthophyll-2, chlorophylls A or B, or alpha-, delta- or gamma-tocopherol or the like; fatty acids, such as 16:0 (palmitic acid), 16:1 (palmitoleic acid), 18:0 (stearic acid), 18:1 (oleic acid), 18:2 (linoleic acid), 20:0 , 18:3 (linolenic acid), 20:1 (eicosenoic acid), 20:2, 22:1 (erucic acid) or the like; waxes, such as by altering the levels of C29, C31, or C33 alkanes; sterols, such as brassicasterol, campesterol, stigmasterol, sitosterol or stigmastanol or the like, glucosinolates, protein or oil levels

Fatty acids were measured using two methods depending on whether the tissue was from leaves or seeds. For leaves, lipids were extracted and esterified with hot methanolic H2SO4 and partitioned into hexane from methanolic brine. For seed fatty acids, seeds were pulverized and extracted in methanol:heptane:toluene:2,2-dimethoxypropane:H2SO4 (39:34:20:5:2) for 90 minutes at 80°C. After cooling to room temperature the upper phase, containing the seed fatty

acid esters, was subjected to GC analysis. Fatty acid esters from both seed and leaf tissues were analyzed with a Supelco SP-2330 column.

Glucosinolates were purified from seeds or leaves by first heating the tissue at 95°C for 10 minutes. Preheated ethanol:water (50:50) is and after heating at 95°C for a further 10 minutes, the extraction solvent is applied to a DEAE Sephadex column which had been previously equilibrated with 0.5 M pyridine acetate. Desulfoglucosinolates were eluted with 300 ul water and analyzed by reverse phase HPLC monitoring at 226 nm.

For wax alkanes, samples were extracted using an identical method as fatty acids and extracts were analyzed on a HP 5890 GC coupled with a 5973 MSD. Samples were chromatographed on a J&W DB35 mass spectrometer (J&W Scientific).

To measure prenyl lipids levels, seeds or leaves were pulverized with 1 to 2% pyrogallol as an antioxidant. For seeds, extracted samples were filtered and a portion removed for tocopherol and carotenoid/chlorophyll analysis by HPLC. The remaining material was saponified for sterol determination. For leaves, an aliquot was removed and diluted with methanol and chlorophyll A, chlorophyll B, and total carotenoids measured by spectrophotometry by determining absorbance at 665.2 nm, 652.5 nm, and 470 nm. An aliquot was removed for tocopherol and carotenoid/chlorophyll composition by HPLC using a Waters uBondapak C18 column (4.6 mm x 150 mm). The remaining methanolic solution was saponified with 10% KOH at 80°C for one hour. The samples were cooled and diluted with a mixture of methanol and water. A solution of 2% methylene chloride in hexane was mixed in and the samples were centrifuged. The aqueous methanol phase was again re-extracted 2% methylene chloride in hexane and, after centrifugation, the two upper phases were combined and evaporated. 2% methylene chloride in hexane was added to the tubes and the samples were then extracted with one ml of water. The upper phase was removed, dried, and resuspended in 400 ul of 2% methylene chloride in hexane and analyzed by gas chromatography using a 50 m DB-5ms (0.25 mm ID, 0.25 um phase, J&W Scientific).

Insoluble sugar levels were measured by the method essentially described by Reiter et al., Plant Journal 12:335-345. This method analyzes the neutral sugar composition of cell wall polymers found in *Arabidopsis* leaves. Soluble sugars were separated from sugar polymers by extracting leaves with hot 70% ethanol. The remaining residue containing the insoluble polysaccharides was then acid hydrolyzed with allose added as an internal standard. Sugar monomers generated by the hydrolysis were then reduced to the corresponding alditols by treatment with NaBH4, then were acetylated to generate the volatile alditol acetates which were then analyzed by GC-FID. Identity of the peaks was determined by comparing the retention times

of known sugars converted to the corresponding alditol acetates with the retention times of peaks from wild-type plant extracts. Alditol acetates were analyzed on a Supelco SP-2330 capillary column (30 m x 250 um x 0.2 um) using a temperature program beginning at 180° C for 2 minutes followed by an increase to 220° C in 4 minutes. After holding at 220° C for 10 minutes, the oven temperature is increased to 240° C in 2 minutes and held at this temperature for 10 minutes and brought back to room temperature.

To identify plants with alterations in total seed oil or protein content, 150mg of seeds from T2 progeny plants were subjected to analysis by Near Infrared Reflectance (NIR) using a Foss NirSystems Model 6500 with a spinning cup transport system.

Table 3 shows the phenotypes observed for particular overexpressor or knockout plants and provides the SEQ ID No., the internal reference code (GID), whether a knockout or overexpressor plant was analyzed and the observed phenotype.

Table 3

GIDs	Knockout (KO) or overexpressor (OE)	Phenotype observed
G214	OE	Up to 111% increase in seed lutein
G226	OE	Up to 17% increase in seed protein content
G229	OE	Up to 11% increase in seed oil, 13% decrease in seed protein
G241	OE	Up to 13% decrease in seed oil
G464	OE	Up to 12% decrease in seed oil, 25% increase in seed protein
G663	OE	Up to 16% decrease in seed oil, 14% increase in seed protein
G776	OE	Up to 31% alteration in some seed fatty acids, including .....
G778	OE	Up to 32% increase in seed 18:1 fatty acid
G865	OE	Up to 39% increase seed protein; 23% increase in seed oil
G869	OE	Up to 25% alteration in some seed fatty acids
G883	OE	Up to 47% decrease in seed lutein
G938	OE	Up to 115% increase in some seed fatty acids
G1328	OE	Up to 43% decrease in seed lutein
G584	OE	Larger seeds
G668	OE	Reduced seed color

For a particular overexpressor that shows a less beneficial seed characteristic, it may be more useful to select a plant with a decreased expression of the particular transcription factor. For a particular knockout that shows a less beneficial seed characteristic, it may be more useful to select a plant with an increased expression of the particular transcription factor.

EXAMPLE VIII. IDENTIFICATION OF HOMOLOGOUS SEQUENCES

Homologous sequences from *Arabidopsis* and plant species other than *Arabidopsis* were identified using database sequence search tools, such as the Basic Local Alignment Search Tool (BLAST) (Altschul et al. (1990) J. Mol. Biol. 215:403-410; and Altschul et al. (1997) Nucl. Acid Res. 25: 3389-3402). The tblastx sequence analysis programs were employed using the BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) Proc. Natl. Acad. Sci. USA 89: 10915-10919).

Identified *Arabidopsis* homologous sequences are provided in Figure 2 and included in the Sequence Listing. The percent sequence identity among these sequences is as low as 47% sequence identity. Additionally, the entire NCBI GenBank database was filtered for sequences from all plants except *Arabidopsis thaliana* by selecting all entries in the NCBI GenBank database associated with NCBI taxonomic ID 33090 (Viridiplantae; all plants) and excluding entries associated with taxonomic ID 3701 (*Arabidopsis thaliana*). These sequences were compared to sequences representing genes of SEQ IDs Nos. 1-54 on 9/26/2000 using the Washington University TBLASTX algorithm (version 2.0a19MP). For each gene of SEQ IDs Nos. 1-54, individual comparisons were ordered by probability score (P-value), where the score reflects the probability that a particular alignment occurred by chance. For example, a score of 3.6e-40 is 3.6×10^{-40}. For up to ten species, the gene with the lowest P-value (and therefore the most likely homolog) is listed in Figure 3.

In addition to P-values, comparisons were also scored by percentage identity. Percentage identity reflects the degree to which two segments of DNA or protein are identical over a particular length. The ranges of percent identity between the non-Arabidopsis genes shown in Figure 3 and the Arabidopsis genes in the sequence listing are: SEQ ID No. 1: 38%-89%; SEQ ID No. 3: 50%-69%; SEQ ID No. 5: 68%-93%; SEQ ID No. 7: 69%-84%; SEQ ID No. 9: 34%-60%; SEQ ID No. 11: 52%-81%; SEQ ID No. 13: 48%-81%; SEQ ID No. 15: 37%-80%; SEQ ID No. 17: 48%-83%; SEQ ID No. 19: 31%-68%; SEQ ID No. 21: 47%-90%; SEQ ID No. 23: 57%-88%; SEQ ID No. 25: 39%-79%; SEQ ID No. 27: 35%-84%; SEQ ID No. 29: 54%-89%; SEQ ID No. 31: 42%-88%; SEQ ID No. 33: 41%-75%; SEQ ID No. 35: 34%-67%; SEQ ID No. 37: 72%-86%; SEQ ID No. 39: 39%-84%; SEQ ID No. 41: 40%-58%; SEQ ID No. 43: 44%-82%; SEQ ID

No. 45: 54%-68%; SEQ ID No. 47: 48%-64%; SEQ ID No. 49: 46%-88%; SEQ ID No. 51: 52%-92%; and SEQ ID No. 53: 48%-80%.

The polynucleotides and polypeptides in the Sequence Listing and the identified homologous sequences may be stored in a computer system and have associated or linked with the sequences a function, such as that the polynucleotides and polypeptides are useful for modifying the seed characteristics of a plant.

All references, publications, patents and other documents herein are incorporated by reference in their entirety for all purposes. Although the invention has been described with reference to the embodiments and examples above, it should be understood that various modifications can be made without departing from the spirit of the invention.

What is claimed is:

1. A transgenic plant with modified seed characteristics, which plant comprises a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-27, or a complementary nucleotide sequence thereof;

(b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);

(c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-1, where N=1-27, or a complementary nucleotide sequence thereof;

(d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);

(e) a nucleotide sequence which hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);

(f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e);

(g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies a plant's seed characteristics;

(h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g);

(i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g);

(j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27;

(k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27; and

(l) a nucleotide sequence which encodes a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-27.

2. The transgenic plant of claim 1, further comprising a constitutive, inducible, or tissue-active promoter operably linked to said nucleotide sequence.

3. The transgenic plant of claim 1, wherein the plant is selected from the group consisting of: soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf,

banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits, and vegetable brassicas.

4. An isolated or recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence encoding a polypeptide comprising a sequence selected from SEQ ID Nos. 2N, where N=1-27, or a complementary nucleotide sequence thereof;

(b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);

(c) a nucleotide sequence comprising a sequence selected from those of SEQ ID Nos. 2N-1, where N=1-27, or a complementary nucleotide sequence thereof;

(d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);

(e) a nucleotide sequence which hybridizes under stringent conditions to a nucleotide sequence of one or more of: (a), (b), (c), or (d);

(f) a nucleotide sequence comprising at least 15 consecutive nucleotides of a sequence of any of (a)-(e);

(g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies a plant's seed characteristics;

(h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g);

(i) a nucleotide sequence having at least 60% identity sequence identity to a nucleotide sequence of any of (a)-(g);

(j) a nucleotide sequence which encodes a polypeptide having at least 31% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27;

(k) a nucleotide sequence which encodes a polypeptide having at least 60% identity sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-27; and

(l) a nucleotide sequence which encodes a conserved domain of a polypeptide having at least 65% sequence identity to a conserved domain of a polypeptide of SEQ ID Nos. 2N, where N=1-27.

5. The isolated or recombinant polynucleotide of claim 4, further comprising a constitutive, inducible, or tissue-active promoter operably linked to the nucleotide sequence.

6. A cloning or expression vector comprising the isolated or recombinant polynucleotide of claim 4.

7. A cell comprising the cloning or expression vector of claim 6.

8. A transgenic plant comprising the isolated or recombinant polynucleotide of claim 4.

9. A composition produced by one or more of:
(a) incubating one or more polynucleotide of claim 4 with a nuclease;
(b) incubating one or more polynucleotide of claim 4 with a restriction enzyme;
(c) incubating one or more polynucleotide of claim 4 with a polymerase;
(d) incubating one or more polynucleotide of claim 4 with a polymerase and a primer;
(e) incubating one or more polynucleotide of claim 4 with a cloning vector, or
(f) incubating one or more polynucleotide of claim 4 with a cell.

10. A composition comprising two or more different polynucleotides of claim 4.

11. An isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4.

12. A plant ectopically expressing an isolated polypeptide of claim 11.

13. A method for producing a plant having a modified seed characteristics, the method comprising altering the expression of the isolated or recombinant polynucleotide of claim 4 or the expression levels or activity of a polypeptide of claim 11 in a plant, thereby producing a modified plant, and selecting the modified plant for improved seed characteristics thereby providing the modified plant with a modified seed characteristics.

14. The method of claim 13, wherein the polynucleotide is a polynucleotide of claim 4.

15. A method of identifying a factor that is modulated by or interacts with a polypeptide encoded by a polynucleotide of claim 4, the method comprising:

(a) expressing a polypeptide encoded by the polynucleotide in a plant; and

(b) identifying at least one factor that is modulated by or interacts with the polypeptide.

16. The method of claim 15, wherein the identifying is performed by detecting binding by the polypeptide to a promoter sequence, or detecting interactions between an additional protein and the polypeptide in a yeast two hybrid system.

17. The method of claim 15, wherein the identifying is performed by detecting expression of a factor by hybridization to a microarray, subtractive hybridization or differential display.

18. A method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide of interest, the method comprising:

(a) placing the molecule in contact with a plant comprising the polynucleotide or polypeptide encoded by the polynucleotide of claim 4; and,

(b) monitoring one or more of:

(i) expression level of the polynucleotide in the plant;

(ii) expression level of the polypeptide in the plant;

(iii) modulation of an activity of the polypeptide in the plant; or

(iv) modulation of an activity of the polynucleotide in the plant.

19. An integrated system, computer or computer readable medium comprising one or more character strings corresponding to a polynucleotide of claim 4, or to a polypeptide encoded by the polynucleotide.

20. The integrated system, computer or computer readable medium of claim 19, further comprising a link between said one or more sequence strings to a modified plant seed characteristics phenotype.

21. A method of identifying a sequence similar or homologous to one or more polynucleotides of claim 4, or one or more polypeptides encoded by the polynucleotides, the method comprising:

(a) providing a sequence database; and,

(b) querying the sequence database with one or more target sequences corresponding to the one or more polynucleotides or to the one or more polypeptides to identify one or more sequence members of the database that display sequence similarity or homology to one or more of the one or more target sequences.

22. The method of claim 21, wherein the querying comprises aligning one or more of the target sequences with one or more of the one or more sequence members in the sequence database.

23. The method of claim 21, wherein the querying comprises identifying one or more of the one or more sequence members of the database that meet a user-selected identity criteria with one or more of the target sequences.

24. The method of claim 21, further comprising linking the one or more of the polynucleotides of claim 4, or encoded polypeptides, to a modified plant seed characteristics phenotype.

25. A plant comprising altered expression levels of an isolated or recombinant polynucleotide of claim 4.

26. A plant comprising altered expression levels or the activity of an isolated or recombinant polypeptide of claim 11.

27. A plant lacking a nucleotide sequence encoding a polypeptide of claim 11.

Figure 1

SEQ ID No.	GID	cDNA or protein	conserved domain
1	G214	cDNA	
2	G214	protein	22-71
3	G226	cDNA	
4	G226	protein	28-78
5	G229	cDNA	
6	G229	protein	14-120
7	G241	cDNA	
8	G241	protein	14-114
9	G464	cDNA	
10	G464	protein	7-15,70-80,125-158,183-219
11	G663	cDNA	
12	G663	protein	9-111
13	G776	cDNA	
14	G776	protein	27-175
15	G778	cDNA	
16	G778	protein	220-267
17	G865	cDNA	
18	G865	protein	36-103
19	G869	cDNA	
20	G869	protein	109-177
21	G883	cDNA	
22	G883	protein	245-302
23	G938	cDNA	
24	G938	protein	96-104
25	G1328	cDNA	
26	G1328	protein	14-119
27	G584	cDNA	
28	G584	protein	401-494
29	G668	cDNA	
30	G668	protein	13-113

Figure 2

SEQ ID No.	GID	homolog	cDNA or protein	conserved domain
31	G680	homolog of G214	cDNA	
32	G680	homolog of G214	protein	24-70
33	G682	homolog of G226	cDNA	
34	G682	homolog of G226	protein	22-53
35	G225	homolog of G226	cDNA	
36	G225	homolog of G226	protein	39-76
37	G678	homolog of G229	cDNA	
38	G678	homolog of G229	protein	14-115
39	G233	homolog of G241	cDNA	
40	G233	homolog of G241	protein	14-114
41	G463	homolog of G464	cDNA	
42	G463	homolog of G464	protein	14-23, 77-88, 130-146, 194-227
43	G2422	homolog of G663	cDNA	
44	G2422	homolog of G663	protein	9-110
45	G2421	homolog of G663	cDNA	
46	G2421	homolog of G663	protein	9-110
47	G772	homolog of G776	cDNA	
48	G772	homolog of G776	protein	27-176
49	G866	homolog of G883	cDNA	
50	G866	homolog of G883	protein	43-300
51	G941	homolog of G938	cDNA	
52	G941	homolog of G938	protein	95-103
53	G198	homolog of G1328	cDNA	
54	G198	homolog of G1328	protein	14-117

Figure 3A

SEQ IDs	Gene Ids	Genbank NID	P-value	Species
1	G214	8170933	8.80E-35	Lycopersicon esculentum
1	G214	9205339	1.20E-27	Glycine max
1	G214	8577344	1.80E-23	Zea mays
1	G214	9119112	2.40E-18	Medicago truncatula
1	G214	7660673	4.80E-15	Sorghum bicolor
1	G214	8213273	4.40E-14	Oryza sativa
1	G214	3325786	4.70E-10	Gossypium hirsutum
1	G214	9435251	1.50E-09	Hordeum vulgare
1	G214	9411569	6.80E-09	Triticum aestivum
1	G214	7614730	3.00E-07	Lotus japonicus
3	G226	4396287	5.10E-15	Glycine max
3	G226	9410205	1.50E-05	Triticum aestivum
3	G226	3857004	0.11	Populus tremula x Populus tremuloides
3	G226	2428139	0.35	Oryza sativa
5	G229	7337390	5.20E-51	Lycopersicon esculentum
5	G229	7244424	3.90E-50	Mentha x piperita
5	G229	7776053	1.30E-49	Lotus japonicus
5	G229	2921335	4.60E-48	Gossypium hirsutum
5	G229	1491932	3.60E-47	Zea mays
5	G229	6455590	2.20E-44	Glycine max
5	G229	6020191	1.60E-41	Pinus taeda
5	G229	7765706	4.10E-41	Medicago truncatula
5	G229	7629167	3.20E-40	Gossypium arboreum
5	G229	6850206	4.30E-40	Oryza sativa
7	G241	6552360	2.60E-54	Nicotiana tabacum
7	G241	6782745	2.20E-53	Oryza sativa
7	G241	8097368	5.70E-53	Hordeum vulgare
7	G241	20560	1.80E-52	Petunia x hybrida
7	G241	7217727	2.70E-52	Sorghum bicolor
7	G241	5891408	4.60E-52	Lycopersicon esculentum
7	G241	5139803	7.40E-52	Glycine max
7	G241	7560175	4.10E-50	Medicago truncatula
7	G241	8381332	1.40E-44	Gossypium arboreum
7	G241	4886263	1.20E-42	Antirrhinum majus
9	G464	6527230	3.60E-31	Lycopersicon esculentum
9	G464	9305572	1.10E-22	Sorghum bicolor
9	G464	6604917	6.70E-22	Medicago truncatula
9	G464	5058123	2.30E-21	Glycine max
9	G464	3760881	1.20E-19	Oryza sativa
9	G464	5044476	1.20E-17	Gossypium hirsutum
9	G464	9412603	6.40E-15	Triticum aestivum
9	G464	7777277	3.20E-13	Lotus japonicus
9	G464	9410371	1.70E-11	Hordeum vulgare
9	G464	7624108	2.10E-10	Gossypium arboreum
11	G663	7673087	4.10E-43	Petunia integrifolia
11	G663	7673091	2.60E-41	Petunia x hybrida
11	G663	7339148	1.30E-39	Lycopersicon esculentum
11	G663	7673097	1.90E-36	Petunia axillaris
11	G663	5048991	9.90E-34	Gossypium hirsutum
11	G663	6455590	2.00E-31	Glycine max
11	G663	7560175	1.50E-27	Medicago truncatula
11	G663	7244424	3.20E-26	Mentha x piperita
11	G663	6020191	2.90E-25	Pinus taeda

Figure 3B

SEQ IDs	Gene Ids	Genbank NID	P-value	Species
11	G663	4138298	3.40E-25	Oryza sativa subsp. indica
13	G776	8578423	5.80E-57	Mesembryanthemum crystallinum
13	G776	7411573	2.40E-52	Lycopersicon esculentum
13	G776	9253340	5.80E-43	Solanum tuberosum
13	G776	8383411	6.00E-43	Euphorbia esula
13	G776	7565426	1.50E-39	Medicago truncatula
13	G776	6666629	2.50E-33	Glycine max
13	G776	6732155	3.60E-33	Triticum monococcum
13	G776	7502501	3.00E-32	Gossypium arboreum
13	G776	8708684	3.80E-32	Hordeum vulgare
13	G776	9307772	2.10E-31	Sorghum bicolor
15	G778	9258500	3.10E-36	Glycine max
15	G778	9211293	9.40E-21	Oryza sativa
15	G778	4380303	7.60E-08	Lycopersicon esculentum
15	G778	7718953	4.10E-07	Medicago truncatula
15	G778	7720768	6.80E-07	Lotus japonicus
15	G778	6536575	8.70E-07	Zea mays
15	G778	1668906	0.82	Citrus sinensis
17	G865	9417297	1.70E-32	Triticum aestivum
17	G865	7206394	4.90E-29	Medicago truncatula
17	G865	7796858	5.70E-27	Glycine max
17	G865	4387560	9.20E-25	Lycopersicon esculentum
17	G865	569065	1.50E-23	Oryza sativa
17	G865	7788764	4.10E-23	Lotus japonicus
17	G865	790362	8.40E-22	Nicotiana tabacum
17	G865	7528275	5.90E-21	Mesembryanthemum crystallinum
17	G865	3264766	8.80E-20	Prunus armeniaca
17	G865	8098026	2.00E-19	Hordeum vulgare
19	G869	2213784	1.30E-19	Lycopersicon esculentum
19	G869	3065894	7.30E-19	Nicotiana tabacum
19	G869	8570080	4.20E-18	Oryza sativa
19	G869	7560260	1.50E-17	Medicago truncatula
19	G869	7534890	5.20E-14	Sorghum bicolor
19	G869	6455322	1.10E-13	Glycine max
19	G869	9362061	2.70E-13	Triticum aestivum
19	G869	7788764	5.70E-13	Lotus japonicus
19	G869	7624302	2.50E-12	Gossypium arboreum
19	G869	3858036	2.80E-12	Populus balsamifera subsp. trichocarpa
21	G883	4760595	2.40E-84	Nicotiana tabacum
21	G883	4894962	3.50E-45	Avena sativa
21	G883	6719425	1.70E-36	Glycine max
21	G883	5273248	2.80E-35	Lycopersicon esculentum
21	G883	9302479	3.00E-34	Sorghum bicolor
21	G883	6799932	1.40E-31	Medicago truncatula
21	G883	5456433	4.30E-31	Zea mays
21	G883	8706346	1.40E-30	Hordeum vulgare
21	G883	8404566	2.70E-30	Oryza sativa
21	G883	1432055	2.00E-27	Petroselinum crispum
23	G938	4239844	3.10E-180	Nicotiana tabacum
23	G938	7739794	2.30E-145	Dianthus caryophyllus
23	G938	7567728	9.60E-98	Medicago truncatula
23	G938	8894549	2.70E-93	Cicer arietinum
23	G938	8104209	9.60E-90	Lycopersicon esculentum

Figure 3C

SEQ IDs	Gene Ids	Genbank NID	P-value	Species
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23	G938	9204568	1.20E-78	Glycine max
23	G938	7720839	1.10E-69	Lotus japonicus
23	G938	7324903	1.60E-52	Lycopersicon pennellii
23	G938	2427923	4.20E-47	Oryza sativa
25	G1328	4383290	5.10E-65	Lycopersicon esculentum
25	G1328	1946266	1.30E-58	Oryza sativa
25	G1328	9264503	1.40E-53	Glycine max
25	G1328	8381332	1.10E-52	Gossypium arboreum
25	G1328	9363004	3.30E-49	Triticum aestivum
25	G1328	7765706	1.90E-47	Medicago truncatula
25	G1328	20562	3.90E-47	Petunia x hybrida
25	G1328	5050757	4.10E-46	Gossypium hirsutum
25	G1328	5860031	7.80E-45	Pinus taeda
25	G1328	4886263	5.30E-44	Antirrhinum majus
27	G584	1142618	2.30E-153	Phaseolus vulgaris
27	G584	4321761	2.40E-128	Zea mays
27	G584	9280727	9.70E-122	Oryza sativa
27	G584	6175251	4.80E-78	Lycopersicon esculentum
27	G584	9193975	2.20E-59	Medicago truncatula
27	G584	9364538	1.40E-53	Triticum aestivum
27	G584	6847033	1.70E-49	Glycine max
27	G584	5049283	8.90E-46	Gossypium hirsutum
27	G584	7781217	1.00E-43	Lotus japonicus
27	G584	4519200	1.20E-27	Perilla frutescens
29	G668	8172976	9.70E-73	Medicago truncatula
29	G668	9252441	1.10E-70	Solanum tuberosum
29	G668	5897694	1.90E-66	Lycopersicon esculentum
29	G668	8380712	7.00E-65	Gossypium arboreum
29	G668	7685936	2.20E-58	Glycine max
29	G668	1945280	4.60E-48	Oryza sativa
29	G668	20562	1.10E-40	Petunia x hybrida
29	G668	7217727	8.20E-37	Sorghum bicolor
29	G668	6552360	1.90E-36	Nicotiana tabacum
29	G668	4886263	5.80E-36	Antirrhinum majus
31	G680	9258166	5.70E-36	Glycine max
31	G680	9255178	3.00E-29	Zea mays
31	G680	5274804	1.20E-27	Lycopersicon esculentum
31	G680	4974199	3.00E-22	Oryza sativa
31	G680	3325786	2.10E-21	Gossypium hirsutum
31	G680	9119112	1.30E-18	Medicago truncatula
31	G680	7660673	3.20E-17	Sorghum bicolor
31	G680	7243970	6.10E-16	Mentha x piperita
31	G680	3858093	2.10E-10	Populus balsamifera subsp. trichocarpa
31	G680	8845091	3.70E-10	Triticum aestivum
33	G682	309571	4.40E-08	Zea mays
33	G682	4396287	1.10E-05	Glycine max
33	G682	3857004	0.00051	Populus tremula x Populus tremuloides
33	G682	9410205	0.00085	Triticum aestivum
33	G682	8382118	0.0079	Gossypium arboreum
33	G682	2428139	0.017	Oryza sativa
33	G682	7339148	0.13	Lycopersicon esculentum
33	G682	9302672	0.32	Sorghum bicolor

Figure 3D

SEQ IDs	Gene Ids	Genbank NID	P-value	Species
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33	G682	6555777	0.46	Pinus taeda
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35	G225	309571	0.00029	Zea mays
35	G225	3857004	0.001	Populus tremula x Populus tremuloides
35	G225	9410205	0.019	Triticum aestivum
35	G225	9426190	0.025	Triticum turgidum subsp. durum
35	G225	8382118	0.046	Gossypium arboreum
35	G225	6782756	0.27	Oryza sativa
35	G225	7721017	0.4	Lotus japonicus
35	G225	6020136	0.47	Pinus taeda
35	G225	2921331	0.48	Gossypium hirsutum
37	G678	7244424	8.70E-50	Mentha x piperita
37	G678	7776053	2.70E-46	Lotus japonicus
37	G678	7337390	2.90E-46	Lycopersicon esculentum
37	G678	2921335	2.30E-43	Gossypium hirsutum
37	G678	6455590	8.30E-43	Glycine max
37	G678	1491932	1.60E-42	Zea mays
37	G678	5860031	4.80E-40	Pinus taeda
37	G678	7765706	3.20E-38	Medicago truncatula
37	G678	6850206	8.20E-38	Oryza sativa
37	G678	7217727	2.00E-37	Sorghum bicolor
39	G233	6552360	6.50E-66	Nicotiana tabacum
39	G233	20560	7.60E-65	Petunia x hybrida
39	G233	5139813	1.70E-58	Glycine max
39	G233	5891103	3.80E-58	Lycopersicon esculentum
39	G233	6782745	1.80E-52	Oryza sativa
39	G233	7560175	1.80E-51	Medicago truncatula
39	G233	7217727	8.30E-51	Sorghum bicolor
39	G233	8097368	5.80E-49	Hordeum vulgare
39	G233	8381332	4.60E-43	Gossypium arboreum
39	G233	5048991	3.50E-41	Gossypium hirsutum
41	G463	6527230	4.90E-36	Lycopersicon esculentum
41	G463	9305572	5.50E-36	Sorghum bicolor
41	G463	3760881	1.20E-31	Oryza sativa
41	G463	6604917	1.30E-23	Medicago truncatula
41	G463	5058123	2.50E-21	Glycine max
41	G463	5044476	1.10E-19	Gossypium hirsutum
41	G463	9412603	1.70E-17	Triticum aestivum
41	G463	9419394	6.00E-17	Hordeum vulgare
41	G463	7624108	6.20E-17	Gossypium arboreum
41	G463	8547152	3.20E-16	Nicotiana tabacum
43	G2422	7673087	9.60E-45	Petunia integrifolia
43	G2422	7339148	6.30E-43	Lycopersicon esculentum
43	G2422	7673083	7.20E-43	Petunia x hybrida
43	G2422	7673097	3.30E-40	Petunia axillaris
43	G2422	5048991	3.30E-36	Gossypium hirsutum
43	G2422	6455590	3.00E-33	Glycine max
43	G2422	6020191	3.20E-32	Pinus taeda
43	G2422	309571	3.60E-30	Zea mays
43	G2422	7560832	9.00E-30	Medicago truncatula
43	G2422	9363004	1.30E-29	Triticum aestivum
45	G2421	7673087	1.10E-46	Petunia integrifolia

Figure 3E

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45	G2421	8380196	7.30E-31	Gossypium arboreum
45	G2421	7673095	1.90E-30	Petunia axillaris
45	G2421	7339148	2.80E-30	Lycopersicon esculentum
45	G2421	8747182	9.00E-30	Medicago truncatula
45	G2421	7217727	1.30E-27	Sorghum bicolor
45	G2421	6073050	5.50E-27	Glycine max
45	G2421	1101769	7.40E-27	Picea mariana
47	G772	8578423	4.80E-58	Mesembryanthemum crystallinum
47	G772	7570276	3.00E-52	Medicago truncatula
47	G772	7411573	1.30E-44	Lycopersicon esculentum
47	G772	6341483	6.30E-33	Glycine max
47	G772	1279639	2.00E-32	Petunia x hybrida
47	G772	7722907	3.50E-32	Lotus japonicus
47	G772	8405571	4.70E-32	Hordeum vulgare
47	G772	6730945	6.40E-32	Oryza sativa
47	G772	9302206	2.50E-31	Sorghum bicolor
47	G772	5047907	1.10E-30	Gossypium hirsutum
49	G866	4760595	3.50E-85	Nicotiana tabacum
49	G866	4894962	1.70E-38	Avena sativa
49	G866	6719425	6.60E-35	Glycine max
49	G866	5273248	1.10E-33	Lycopersicon esculentum
49	G866	9302479	7.40E-33	Sorghum bicolor
49	G866	6799932	3.60E-31	Medicago truncatula
49	G866	4886128	4.50E-31	Zea mays
49	G866	8404566	1.40E-29	Oryza sativa
49	G866	8706346	1.10E-28	Hordeum vulgare
49	G866	1432055	3.50E-26	Petroselinum crispum
51	G941	4239844	3.80E-198	Nicotiana tabacum
51	G941	7739794	1.20E-141	Dianthus caryophyllus
51	G941	7567728	7.10E-102	Medicago truncatula
51	G941	8104209	3.70E-97	Lycopersicon esculentum
51	G941	8894549	2.10E-95	Cicer arietinum
51	G941	5606033	1.60E-79	Glycine max
51	G941	6462339	4.60E-79	Gossypium hirsutum
51	G941	7720839	6.60E-70	Lotus japonicus
51	G941	7324903	1.00E-55	Lycopersicon pennellii
51	G941	2427923	6.90E-47	Oryza sativa
53	G198	4383290	3.50E-64	Lycopersicon esculentum
53	G198	1946266	1.10E-58	Oryza sativa
53	G198	9363004	5.40E-51	Triticum aestivum
53	G198	8381332	6.40E-51	Gossypium arboreum
53	G198	9264503	1.30E-50	Glycine max
53	G198	5050757	4.10E-46	Gossypium hirsutum
53	G198	20562	9.30E-46	Petunia x hybrida
53	G198	7765706	2.70E-45	Medicago truncatula
53	G198	5860031	5.40E-45	Pinus taeda
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35 40 45

ctc atc tct cga atg tac aga ctt gtc ggt aat agg tgg gat tta ata 195
Leu Ile Ser Arg Met Tyr Arg Leu Val Gly Asn Arg Trp Asp Leu Ile
50 55 60

gca gga aga gtc gta gga aga aag gca aat gag att gag aga tac tgg 243
Ala Gly Arg Val Val Gly Arg Lys Ala Asn Glu Ile Glu Arg Tyr Trp
65 70 75

att atg aga aac tct gac tat ttt tct cac aaa cga cga cgt ctt aat 291
Ile Met Arg Asn Ser Asp Tyr Phe Ser His Lys Arg Arg Arg Leu Asn
80 85 90

aat tct ccc ttt ttt tct act tct cct ctt aat ctc caa gaa aat cta 339
Asn Ser Pro Phe Phe Ser Thr Ser Pro Leu Asn Leu Gln Glu Asn Leu
95 100 105 110

aaa ttg taa agaaatcaaa ataaaagctt tcaatcataa aagtagaaca 388
Lys Leu

aatcttgaat gtcttctca 407

<210> 4
<211> 112
<212> PRT
<213> Arabidopsis thaliana

<400> 4

Met Asp Asn Thr Asn Arg Leu Arg Leu Arg Arg Gly Pro Ser Leu Arg
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Gln Thr Lys Phe Thr Arg Ser Arg Tyr Asp Ser Glu Glu Val Ser Ser
20 25 30

Ile Glu Trp Glu Phe Ile Ser Met Thr Glu Gln Glu Glu Asp Leu Ile
35 40 45

Ser Arg Met Tyr Arg Leu Val Gly Asn Arg Trp Asp Leu Ile Ala Gly
50 55 60

Arg Val Val Gly Arg Lys Ala Asn Glu Ile Glu Arg Tyr Trp Ile Met
65 70 75 80

Arg Asn Ser Asp Tyr Phe Ser His Lys Arg Arg Arg Leu Asn Asn Ser
85 90 95

Pro Phe Phe Ser Thr Ser Pro Leu Asn Leu Gln Glu Asn Leu Lys Leu
100 105 110

MBI-17 Sequence Listing.ST25

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                                              1               5

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Cys Cys Glu Lys Val Gly Ile Lys Arg Gly Arg Trp Thr Ala Glu Glu
            10                  15                  20

gac cag att ctc tcc aac tac att caa tcc aat ggt gaa ggt tct tgg      151
Asp Gln Ile Leu Ser Asn Tyr Ile Gln Ser Asn Gly Glu Gly Ser Trp
        25                  30                  35

aga tct ctc ccc aaa aat gcc gga tta aaa agg tgt gga aag agc tgt      199
Arg Ser Leu Pro Lys Asn Ala Gly Leu Lys Arg Cys Gly Lys Ser Cys
    40                  45                  50

aga ttg aga tgg ata aac tat cta aga tca gac ctc aag cgt gga aac      247
Arg Leu Arg Trp Ile Asn Tyr Leu Arg Ser Asp Leu Lys Arg Gly Asn
55                  60                  65

ata act cca gaa gaa gaa gaa ctc gtt gtt aaa ttg cat tcc act ttg      295
Ile Thr Pro Glu Glu Glu Glu Leu Val Val Lys Leu His Ser Thr Leu
70                  75                  80                  85

gga aac agg tgg tca cta atc gcg ggt cat cta cca ggg aga aca gac      343
Gly Asn Arg Trp Ser Leu Ile Ala Gly His Leu Pro Gly Arg Thr Asp
            90                  95                  100

aac gaa ata aaa aat tat tgg aac tct cat ctc agc cgt aaa ctc cac      391
Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu Ser Arg Lys Leu His
        105                 110                 115

aac ttc att agg aag cca tcc atc tct caa gac gtc tcc gcc gta atc      439
Asn Phe Ile Arg Lys Pro Ser Ile Ser Gln Asp Val Ser Ala Val Ile
    120                 125                 130

atg gcg aac gct tct tca gcg cca ccg ccg ccg cag gca aaa cgc aga      487
Met Ala Asn Ala Ser Ser Ala Pro Pro Pro Pro Gln Ala Lys Arg Arg
135                 140                 145

ctt ggg aga acg agt agg tcc gct atg aaa cca aaa atc cgc aga aca      535
Leu Gly Arg Thr Ser Arg Ser Ala Met Lys Pro Lys Ile Arg Arg Thr
150                 155                 160                 165

aaa act cgt aaa acg aag aaa acg tct gca cca ccg gag cct aac gcc      583
Lys Thr Arg Lys Thr Lys Lys Thr Ser Ala Pro Pro Glu Pro Asn Ala
            170                 175                 180

gat gta gct ggg gct gat aaa gaa gca tta atg gtg gag tca agt gga      631
Asp Val Ala Gly Ala Asp Lys Glu Ala Leu Met Val Glu Ser Ser Gly
        185                 190                 195

gcc gag gct gag cta gga cga cca tgt gac tac tat gga gat gat tgt      679
Ala Glu Ala Glu Leu Gly Arg Pro Cys Asp Tyr Tyr Gly Asp Asp Cys
    200                 205                 210

aac aaa aat ctc atg agc att aat ggc gat aat gga gtt tta acg ttt      727
Asn Lys Asn Leu Met Ser Ile Asn Gly Asp Asn Gly Val Leu Thr Phe
215                 220                 225

gat gat gat atc atc gat ctt ttg ttg gac gag tca gat cct ggc cac      775
Asp Asp Asp Ile Ile Asp Leu Leu Leu Asp Glu Ser Asp Pro Gly His
230                 235                 240                 245
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ttg tac aca aac aca acg tgc ggt ggt ggt ggg gag ttg cat aac ata      823
Leu Tyr Thr Asn Thr Thr Cys Gly Gly Gly Gly Glu Leu His Asn Ile
                250                 255                 260

aga gac tct gaa gga gcc aga ggg ttc tcg gat act tgg aac caa ggg      871
Arg Asp Ser Glu Gly Ala Arg Gly Phe Ser Asp Thr Trp Asn Gln Gly
            265                 270                 275

aat ctc gac tgt ctt ctt cag tct tgt cca tct gtg gag tcg ttt ctc      919
Asn Leu Asp Cys Leu Leu Gln Ser Cys Pro Ser Val Glu Ser Phe Leu
        280                 285                 290

aac tac gac cac caa gtt aac gac gcg tcg acg gat gag ttt atc gat      967
Asn Tyr Asp His Gln Val Asn Asp Ala Ser Thr Asp Glu Phe Ile Asp
    295                 300                 305

tgg gat tgt gtt tgg caa gaa ggt agt gat aat aat ctt tgg cat gag     1015
Trp Asp Cys Val Trp Gln Glu Gly Ser Asp Asn Asn Leu Trp His Glu
310                 315                 320                 325

aaa gag aat ccc gac tca atg gtc tcg tgg ctt tta gac ggt gat gat     1063
Lys Glu Asn Pro Asp Ser Met Val Ser Trp Leu Leu Asp Gly Asp Asp
                330                 335                 340

gag gcc acg atc ggg aat agt aat tgt gag aac ttt gga gaa ccg tta     1111
Glu Ala Thr Ile Gly Asn Ser Asn Cys Glu Asn Phe Gly Glu Pro Leu
            345                 350                 355

gat cat gac gac gaa agc gct ttg gtc gct tgg ctt ctg tca tga         1156
Asp His Asp Asp Glu Ser Ala Leu Val Ala Trp Leu Leu Ser
        360                 365                 370

tgatattgat tgatccgtta tgtaatcttt tttgtgcatt cacagtttga atc          1209
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<210> 6
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<213> Arabidopsis thaliana

<400> 6

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Gly Glu Gly Ser Trp Arg Ser Leu Pro Lys Asn Ala Gly Leu Lys Arg
        35                  40                  45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Ser Asp
    50                  55                  60

Leu Lys Arg Gly Asn Ile Thr Pro Glu Glu Glu Glu Leu Val Val Lys
65                  70                  75                  80

Leu His Ser Thr Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly His Leu
                85                  90                  95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu
            100                 105                 110

Ser Arg Lys Leu His Asn Phe Ile Arg Lys Pro Ser Ile Ser Gln Asp
        115                 120                 125
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Val Ser Ala Val Ile Met Ala Asn Ala Ser Ser Ala Pro Pro Pro Pro
130 135 140

Gln Ala Lys Arg Arg Leu Gly Arg Thr Ser Arg Ser Ala Met Lys Pro
145 150 155 160

Lys Ile Arg Arg Thr Lys Thr Arg Lys Thr Lys Lys Thr Ser Ala Pro
165 170 175

Pro Glu Pro Asn Ala Asp Val Ala Gly Ala Asp Lys Glu Ala Leu Met
180 185 190

Val Glu Ser Ser Gly Ala Glu Ala Glu Leu Gly Arg Pro Cys Asp Tyr
195 200 205

Tyr Gly Asp Asp Cys Asn Lys Asn Leu Met Ser Ile Asn Gly Asp Asn
210 215 220

Gly Val Leu Thr Phe Asp Asp Asp Ile Ile Asp Leu Leu Leu Asp Glu
225 230 235 240

Ser Asp Pro Gly His Leu Tyr Thr Asn Thr Thr Cys Gly Gly Gly Gly
245 250 255

Glu Leu His Asn Ile Arg Asp Ser Glu Gly Ala Arg Gly Phe Ser Asp
260 265 270

Thr Trp Asn Gln Gly Asn Leu Asp Cys Leu Leu Gln Ser Cys Pro Ser
275 280 285

Val Glu Ser Phe Leu Asn Tyr Asp His Gln Val Asn Asp Ala Ser Thr
290 295 300

Asp Glu Phe Ile Asp Trp Asp Cys Val Trp Gln Glu Gly Ser Asp Asn
305 310 315 320

Asn Leu Trp His Glu Lys Glu Asn Pro Asp Ser Met Val Ser Trp Leu
325 330 335

Leu Asp Gly Asp Asp Glu Ala Thr Ile Gly Asn Ser Asn Cys Glu Asn
340 345 350

Phe Gly Glu Pro Leu Asp His Asp Asp Glu Ser Ala Leu Val Ala Trp
355 360 365

Leu Leu Ser
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<211> 1046
<212> DNA
<213> Arabidopsis thaliana

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<223> G241

MBI-17 Sequence Listing.ST25

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                                                  Met Gly Arg Ala
                                                  1

cca tgc tgt gag aag atg ggg ttg aag aga gga cca tgg aca cct gaa      105
Pro Cys Cys Glu Lys Met Gly Leu Lys Arg Gly Pro Trp Thr Pro Glu
5                   10                  15                  20

gaa gat caa atc ttg gtc tct ttt atc ctc aac cat gga cat agt aac      153
Glu Asp Gln Ile Leu Val Ser Phe Ile Leu Asn His Gly His Ser Asn
                25                  30                  35

tgg cga gcc ctc cct aag caa gct ggt ctt ttg aga tgt gga aaa agc      201
Trp Arg Ala Leu Pro Lys Gln Ala Gly Leu Leu Arg Cys Gly Lys Ser
            40                  45                  50

tgt aga ctt agg tgg atg aac tat tta aag cct gat att aaa cgt ggc      249
Cys Arg Leu Arg Trp Met Asn Tyr Leu Lys Pro Asp Ile Lys Arg Gly
        55                  60                  65

aat ttc acc aaa gaa gag gaa gat gct atc atc agc tta cac caa ata      297
Asn Phe Thr Lys Glu Glu Glu Asp Ala Ile Ile Ser Leu His Gln Ile
    70                  75                  80

ctt ggc aat aga tgg tca gcg att gca gca aaa ctg cct gga aga acc      345
Leu Gly Asn Arg Trp Ser Ala Ile Ala Ala Lys Leu Pro Gly Arg Thr
85                  90                  95                  100

gat aac gag atc aag aac gta tgg cac act cac ttg aag aag aga ctc      393
Asp Asn Glu Ile Lys Asn Val Trp His Thr His Leu Lys Lys Arg Leu
                105                 110                 115

gaa gat tat caa cca gct aaa cct aag acc agc aac aaa aag aag ggt      441
Glu Asp Tyr Gln Pro Ala Lys Pro Lys Thr Ser Asn Lys Lys Lys Gly
            120                 125                 130

act aaa cca aaa tct gaa tcc gta ata acg agc tcg aac agt act aga      489
Thr Lys Pro Lys Ser Glu Ser Val Ile Thr Ser Ser Asn Ser Thr Arg
        135                 140                 145

agc gaa tcg gag cta gca gat tca tca aac cct tct gga gaa agc tta      537
Ser Glu Ser Glu Leu Ala Asp Ser Ser Asn Pro Ser Gly Glu Ser Leu
    150                 155                 160

ttt tcg aca tcg cct tcg aca agt gag gtt tct tcg atg aca ctc ata      585
Phe Ser Thr Ser Pro Ser Thr Ser Glu Val Ser Ser Met Thr Leu Ile
165                 170                 175                 180

agc cac gac ggc tat agc aac gag att aat atg gat aac aaa ccg gga      633
Ser His Asp Gly Tyr Ser Asn Glu Ile Asn Met Asp Asn Lys Pro Gly
                185                 190                 195

gat atc agt act atc gat caa gaa tgt gtt tct ttc gaa act ttt ggt      681
Asp Ile Ser Thr Ile Asp Gln Glu Cys Val Ser Phe Glu Thr Phe Gly
            200                 205                 210

gcg gat atc gat gaa agc ttc tgg aaa gag aca ctg tat agc caa gat      729
Ala Asp Ile Asp Glu Ser Phe Trp Lys Glu Thr Leu Tyr Ser Gln Asp
        215                 220                 225

gaa cac aac tac gta tcg aat gac cta gaa gtc gct ggt tta gtt gag      777
Glu His Asn Tyr Val Ser Asn Asp Leu Glu Val Ala Gly Leu Val Glu
    230                 235                 240

ata caa caa gag ttt caa aac ttg ggc tcc gct aat aat gag atg att      825
Ile Gln Gln Glu Phe Gln Asn Leu Gly Ser Ala Asn Asn Glu Met Ile
245                 250                 255                 260

ttt gac agt gag atg gaa ctt ctg gtt cga tgt att ggc tag              867
Phe Asp Ser Glu Met Glu Leu Leu Val Arg Cys Ile Gly
                265                 270

aaccggcggg gaacaagatc tcttagccgg gctctagtta acatgtttga ggagtaaagt    927
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gaaatggtgc aaattagtta aggctaagaa attcaaaagc ttttgtttac cgagaaaaaa 987

acacactcta actcttgatg tgatgtagtt agtgtattaa ttagaggctg cgttttcaa 1046

<210> 8
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<212> PRT
<213> Arabidopsis thaliana

<400> 8

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Trp Thr Pro Glu Glu Asp Gln Ile Leu Val Ser Phe Ile Leu Asn His
20 25 30

Gly His Ser Asn Trp Arg Ala Leu Pro Lys Gln Ala Gly Leu Leu Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Lys Pro Asp
50 55 60

Ile Lys Arg Gly Asn Phe Thr Lys Glu Glu Glu Asp Ala Ile Ile Ser
65 70 75 80

Leu His Gln Ile Leu Gly Asn Arg Trp Ser Ala Ile Ala Ala Lys Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp His Thr His Leu
100 105 110

Lys Lys Arg Leu Glu Asp Tyr Gln Pro Ala Lys Pro Lys Thr Ser Asn
115 120 125

Lys Lys Lys Gly Thr Lys Pro Lys Ser Glu Ser Val Ile Thr Ser Ser
130 135 140

Asn Ser Thr Arg Ser Glu Ser Glu Leu Ala Asp Ser Ser Asn Pro Ser
145 150 155 160

Gly Glu Ser Leu Phe Ser Thr Ser Pro Ser Thr Ser Glu Val Ser Ser
165 170 175

Met Thr Leu Ile Ser His Asp Gly Tyr Ser Asn Glu Ile Asn Met Asp
180 185 190

Asn Lys Pro Gly Asp Ile Ser Thr Ile Asp Gln Glu Cys Val Ser Phe
195 200 205

Glu Thr Phe Gly Ala Asp Ile Asp Glu Ser Phe Trp Lys Glu Thr Leu
210 215 220

Tyr Ser Gln Asp Glu His Asn Tyr Val Ser Asn Asp Leu Glu Val Ala
225 230 235 240

Gly Leu Val Glu Ile Gln Gln Glu Phe Gln Asn Leu Gly Ser Ala Asn
245 250 255

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Asn Glu Met Ile Phe Asp Ser Glu Met Glu Leu Leu Val Arg Cys Ile
            260                 265                 270

Gly
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<210> 9
<211> 989
<212> DNA
<213> Arabidopsis thaliana

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<222> (41)..(664)
<223> G464

<400> 9

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Glu Leu Glu Val Gly Lys Ser Asn Leu Pro Ala Glu Ser Glu Leu Glu
                10                  15                  20

ttg gga tta ggg ctc agc ctc ggt ggt ggc gcg tgg aaa gag cgt ggg      151
Leu Gly Leu Gly Leu Ser Leu Gly Gly Gly Ala Trp Lys Glu Arg Gly
            25                  30                  35

agg att ctt act gct aag gat ttt cct tcc gtt ggg tct aaa cgc tct      199
Arg Ile Leu Thr Ala Lys Asp Phe Pro Ser Val Gly Ser Lys Arg Ser
        40                  45                  50

gct gaa tct tcc tct cac caa gga gct tct cct cct cgt tca agt caa      247
Ala Glu Ser Ser Ser His Gln Gly Ala Ser Pro Pro Arg Ser Ser Gln
    55                  60                  65

gtg gta gga tgg cca cca att ggg tta cac agg atg aac agt ttg gtt      295
Val Val Gly Trp Pro Pro Ile Gly Leu His Arg Met Asn Ser Leu Val
70                  75                  80                  85

aat aac caa gct atg aag gca gca aga gcg gaa gaa gga gac ggg gag      343
Asn Asn Gln Ala Met Lys Ala Ala Arg Ala Glu Glu Gly Asp Gly Glu
                90                  95                  100

aag aaa gtt gtg aag aat ggt gag ctc aaa gat gtg tca atg aag gtg      391
Lys Lys Val Val Lys Asn Gly Glu Leu Lys Asp Val Ser Met Lys Val
            105                 110                 115

aat ccg aaa gtt cag ggc tta ggg ttt gtt aag gtg aat atg gat gga      439
Asn Pro Lys Val Gln Gly Leu Gly Phe Val Lys Val Asn Met Asp Gly
        120                 125                 130

gtt ggt ata ggc aga aaa gtg gat atg aga gct cat tcg tct tac gaa      487
Val Gly Ile Gly Arg Lys Val Asp Met Arg Ala His Ser Ser Tyr Glu
    135                 140                 145

aac ttg gct cag acg ctt gag gaa atg ttc ttt gga atg aca ggt act      535
Asn Leu Ala Gln Thr Leu Glu Glu Met Phe Phe Gly Met Thr Gly Thr
150                 155                 160                 165

act tgt cga gaa acg gtt aaa cct tta agg ctt tta gat gga tca tca      583
Thr Cys Arg Glu Thr Val Lys Pro Leu Arg Leu Leu Asp Gly Ser Ser
                170                 175                 180

gac ttt gta ctc act tat gaa gat aag ggg att gga tgc ttg ttg gag      631
Asp Phe Val Leu Thr Tyr Glu Asp Lys Gly Ile Gly Cys Leu Leu Glu
            185                 190                 195

atg ttc cat gga gaa tgt tta tca act cgg tga aaaggcttcg gatcatggga    684
Met Phe His Gly Glu Cys Leu Ser Thr Arg
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200 205

acctcagaag ctagtggact agctccaaga cgtcaagagc agaaggatag acaaagaaac 744

aaccctgttt agcttccctt ccaaagctgg cattgtttat gtattgtttg aggtttgcaa 804

tttactcgat acttttttgaa gaaagtattt tggagaatat ggataaaagc atgcagaagc 864

ttagatatga tttgaatccg gttttcggat atggttttgc ttaggtcatt caattcgtag 924

ttttccagtt tgtttcttct ttggctgtgt accaattatc tatgttctgt gagagaaagc 984

tcttg 989

<210> 10
<211> 207
<212> PRT
<213> Arabidopsis thaliana

<400> 10

Met Arg Gly Val Ser Glu Leu Glu Val Gly Lys Ser Asn Leu Pro Ala
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Glu Ser Glu Leu Glu Leu Gly Leu Gly Leu Ser Leu Gly Gly Gly Ala
20 25 30

Trp Lys Glu Arg Gly Arg Ile Leu Thr Ala Lys Asp Phe Pro Ser Val
35 40 45

Gly Ser Lys Arg Ser Ala Glu Ser Ser Ser His Gln Gly Ala Ser Pro
50 55 60

Pro Arg Ser Ser Gln Val Val Gly Trp Pro Pro Ile Gly Leu His Arg
65 70 75 80

Met Asn Ser Leu Val Asn Asn Gln Ala Met Lys Ala Ala Arg Ala Glu
85 90 95

Glu Gly Asp Gly Glu Lys Lys Val Val Lys Asn Gly Glu Leu Lys Asp
100 105 110

Val Ser Met Lys Val Asn Pro Lys Val Gln Gly Leu Gly Phe Val Lys
115 120 125

Val Asn Met Asp Gly Val Gly Ile Gly Arg Lys Val Asp Met Arg Ala
130 135 140

His Ser Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu Glu Met Phe Phe
145 150 155 160

Gly Met Thr Gly Thr Thr Cys Arg Glu Thr Val Lys Pro Leu Arg Leu
165 170 175

Leu Asp Gly Ser Ser Asp Phe Val Leu Thr Tyr Glu Asp Lys Gly Ile
180 185 190

Gly Cys Leu Leu Glu Met Phe His Gly Glu Cys Leu Ser Thr Arg
195 200 205

<210> 11

MBI-17 Sequence Listing.ST25

<211> 1033
<212> DNA
<213> Arabidopsis thaliana

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<222> (113)..(862)
<223> G663

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Met Glu
1

ggt tcg tcc aaa ggg ttg agg aaa ggt gca tgg act gct gaa gaa gat 166
Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu Glu Asp
5 10 15

agt ctc ttg agg cta tgt att gat aag tat gga gaa ggc aaa tgg cat 214
Ser Leu Leu Arg Leu Cys Ile Asp Lys Tyr Gly Glu Gly Lys Trp His
20 25 30

caa gtt cct ttg aga gct ggg cta aat cga tgc aga aag agt tgt aga 262
Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser Cys Arg
35 40 45 50

cta aga tgg ttg aac tat ttg aag cca agt atc aag aga gga aga ctt 310
Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly Arg Leu
55 60 65

agc aat gat gaa gtt gat ctt ctt ctt cgc ctt cat aag ctt cta gga 358
Ser Asn Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu Leu Gly
70 75 80

aat agg tgg tcc ttg att gct ggt cga ttg cct ggt cgg acc gct aat 406
Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr Ala Asn
85 90 95

gat gtc aaa aat tac tgg aac acc cat ctg agt aaa aaa cat gag tct 454
Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His Glu Ser
100 105 110

tcg tgt tgt aag tct aaa atg aaa aag aaa aac att att tcc cct cct 502
Ser Cys Cys Lys Ser Lys Met Lys Lys Lys Asn Ile Ile Ser Pro Pro
115 120 125 130

aca aca ccg gtc caa aaa atc ggt gtt ttt aag cct cga cct cga tcc 550
Thr Thr Pro Val Gln Lys Ile Gly Val Phe Lys Pro Arg Pro Arg Ser
135 140 145

ttc tct gtt aac aat ggt tgc agc cat ctc aat ggt ctg cca gaa gtt 598
Phe Ser Val Asn Asn Gly Cys Ser His Leu Asn Gly Leu Pro Glu Val
150 155 160

gat tta att cct tca tgc ctt gga ctc aag aaa aat aat gtt tgt gaa 646
Asp Leu Ile Pro Ser Cys Leu Gly Leu Lys Lys Asn Asn Val Cys Glu
165 170 175

aat agt atc aca tgt aac aaa gat gat gag aaa gat gat ttt gtg aat 694
Asn Ser Ile Thr Cys Asn Lys Asp Asp Glu Lys Asp Asp Phe Val Asn
180 185 190

aat cta atg aat gga gat aat atg tgg ttg gag aat tta ctg ggg gaa 742
Asn Leu Met Asn Gly Asp Asn Met Trp Leu Glu Asn Leu Leu Gly Glu
195 200 205 210

aac caa gaa gct gat gcg att gtt cct gaa gcg acg aca gct gaa cat 790
Asn Gln Glu Ala Asp Ala Ile Val Pro Glu Ala Thr Thr Ala Glu His
215 220 225

ggg gcc act ttg gcg ttt gac gtt gag caa ctt tgg agt ctg ttt gat 838
Gly Ala Thr Leu Ala Phe Asp Val Glu Gln Leu Trp Ser Leu Phe Asp

230 235 240

gga gag act gtt gaa ctt gat tag tgtttctcac cgtttgttta agattgtggg 892
Gly Glu Thr Val Glu Leu Asp
245

tggctttttct ttcgtatttt agtaatgtat ttttctgtat gaagtaaaga atttcagcat 952

tttaagaaaa atggttatgt ttctacgtaa taaaaaaaaa cgttatttat aaaaaaaaaa 1012

aaaaaaaaaa aaaaaaaaaa a 1033

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<212> PRT
<213> Arabidopsis thaliana

<400> 12

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1 5 10 15

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20 25 30

Trp His Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
35 40 45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
50 55 60

Arg Leu Ser Asn Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu
65 70 75 80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
85 90 95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
100 105 110

Glu Ser Ser Cys Cys Lys Ser Lys Met Lys Lys Lys Asn Ile Ile Ser
115 120 125

Pro Pro Thr Thr Pro Val Gln Lys Ile Gly Val Phe Lys Pro Arg Pro
130 135 140

Arg Ser Phe Ser Val Asn Asn Gly Cys Ser His Leu Asn Gly Leu Pro
145 150 155 160

Glu Val Asp Leu Ile Pro Ser Cys Leu Gly Leu Lys Lys Asn Asn Val
165 170 175

Cys Glu Asn Ser Ile Thr Cys Asn Lys Asp Asp Glu Lys Asp Asp Phe
180 185 190

Val Asn Asn Leu Met Asn Gly Asp Asn Met Trp Leu Glu Asn Leu Leu
195 200 205

Gly Glu Asn Gln Glu Ala Asp Ala Ile Val Pro Glu Ala Thr Thr Ala
210 215 220

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Glu His Gly Ala Thr Leu Ala Phe Asp Val Glu Gln Leu Trp Ser Leu
225                 230                 235                 240

Phe Asp Gly Glu Thr Val Glu Leu Asp
                245
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<211> 1640
<212> DNA
<213> Arabidopsis thaliana

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<221> CDS
<222> (76)..(1431)
<223> G776

<400> 13

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                Met Gly Arg Glu Ser Val Ala Val Val Thr Ala Pro
                1               5                   10

ccc tcg gcg act gct ccg ggt act gct tcg gtg gcg acc tcg ctt gct     159
Pro Ser Ala Thr Ala Pro Gly Thr Ala Ser Val Ala Thr Ser Leu Ala
        15                  20                  25

cct ggc ttc cga ttt cat ccg act gat gag gaa ctc gtg agc tat tac     207
Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Val Ser Tyr Tyr
    30                  35                  40

ttg aag agg aag gtt ctg ggc caa cct gta cgc ttc gat gcg att gga     255
Leu Lys Arg Lys Val Leu Gly Gln Pro Val Arg Phe Asp Ala Ile Gly
45                  50                  55                  60

gag gtc gat ata tac aag cat gag ccc tgg gat tta gca gtg ttt tcg     303
Glu Val Asp Ile Tyr Lys His Glu Pro Trp Asp Leu Ala Val Phe Ser
                65                  70                  75

aga ttg aag aca agg gac caa gaa tgg tac ttc tac agt gca tta gat     351
Arg Leu Lys Thr Arg Asp Gln Glu Trp Tyr Phe Tyr Ser Ala Leu Asp
            80                  85                  90

aag aag tat gga aac ggt gct agg atg aac cga gca act aac aga ggg     399
Lys Lys Tyr Gly Asn Gly Ala Arg Met Asn Arg Ala Thr Asn Arg Gly
        95                  100                 105

tac tgg aaa gct act gga aaa gac aga gaa atc cgc cgt gac att ctg     447
Tyr Trp Lys Ala Thr Gly Lys Asp Arg Glu Ile Arg Arg Asp Ile Leu
    110                 115                 120

ctt ctc ggt atg aaa aag aca ctt gtt ttc cac agt ggg cgt gca cca     495
Leu Leu Gly Met Lys Lys Thr Leu Val Phe His Ser Gly Arg Ala Pro
125                 130                 135                 140

gac ggg ctt cgg act aat tgg gtt atg cat gag tat cgc ctt gtg gaa     543
Asp Gly Leu Arg Thr Asn Trp Val Met His Glu Tyr Arg Leu Val Glu
                145                 150                 155

tat gaa acc gag aaa aac gga aac ctg gtg caa gat gca tat gtg ttg     591
Tyr Glu Thr Glu Lys Asn Gly Asn Leu Val Gln Asp Ala Tyr Val Leu
            160                 165                 170

tgt aga gtc ttc cac aag aat aac att ggg cca cca agt ggg aac aga     639
Cys Arg Val Phe His Lys Asn Asn Ile Gly Pro Pro Ser Gly Asn Arg
        175                 180                 185

tat gct ccg ttc atg gaa gag gaa tgg gct gat gat gaa gga gct ctg     687
Tyr Ala Pro Phe Met Glu Glu Glu Trp Ala Asp Asp Glu Gly Ala Leu
    190                 195                 200
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att cca gga ata gac gtt aag ctc agg cta gag ccg ccg cca gta gcc      735
Ile Pro Gly Ile Asp Val Lys Leu Arg Leu Glu Pro Pro Pro Val Ala
205                 210                 215                 220

aat gga aac gac cag atg gac cag gaa atc cag tca gcc agc aag agt      783
Asn Gly Asn Asp Gln Met Asp Gln Glu Ile Gln Ser Ala Ser Lys Ser
                225                 230                 235

ctc atc aac atc aat gag cca ccg aga gag aca gct cca ctg gat atc      831
Leu Ile Asn Ile Asn Glu Pro Pro Arg Glu Thr Ala Pro Leu Asp Ile
            240                 245                 250

gaa tcg gac caa cag aat cat cat gag aat gac ctc aag ccg gag gag      879
Glu Ser Asp Gln Gln Asn His His Glu Asn Asp Leu Lys Pro Glu Glu
        255                 260                 265

cat aac aac aat aat aat tat gat gaa aac gag gaa aca ctc aaa cgc      927
His Asn Asn Asn Asn Asn Tyr Asp Glu Asn Glu Glu Thr Leu Lys Arg
    270                 275                 280

gag cag atg gaa gaa gag gag cgt cct cct cga cct gta tgc gtt ctc      975
Glu Gln Met Glu Glu Glu Glu Arg Pro Pro Arg Pro Val Cys Val Leu
285                 290                 295                 300

aac aaa gaa gct cca tta cct ctt ctg caa tac aaa cgt aga cgc caa     1023
Asn Lys Glu Ala Pro Leu Pro Leu Leu Gln Tyr Lys Arg Arg Arg Gln
                305                 310                 315

agc gag tcc aac aac aac tca agc agg aac aca cag gac cat tgt tcg     1071
Ser Glu Ser Asn Asn Asn Ser Ser Arg Asn Thr Gln Asp His Cys Ser
            320                 325                 330

tcc aca aca aca act gtc gac aat aca acc act tta atc tca tca tct     1119
Ser Thr Thr Thr Thr Val Asp Asn Thr Thr Thr Leu Ile Ser Ser Ser
        335                 340                 345

gcc gct gcc acc aac act gcc atc tct gca ttg ctt gag ttc tca ctc     1167
Ala Ala Ala Thr Asn Thr Ala Ile Ser Ala Leu Leu Glu Phe Ser Leu
    350                 355                 360

atg ggt atc tcc gac aag aaa gaa aag ccg cag caa ccg cta cgt cct     1215
Met Gly Ile Ser Asp Lys Lys Glu Lys Pro Gln Gln Pro Leu Arg Pro
365                 370                 375                 380

cac aag gaa cct ttg cct cct caa act cca ctt gca tct cct gaa gag     1263
His Lys Glu Pro Leu Pro Pro Gln Thr Pro Leu Ala Ser Pro Glu Glu
                385                 390                 395

aag gtt aat gat ctc cag aag gag att cac cag atg tct gtt gaa aga     1311
Lys Val Asn Asp Leu Gln Lys Glu Ile His Gln Met Ser Val Glu Arg
            400                 405                 410

gaa act ttc aag ctt gaa atg atg agt gca gaa gct atg atc agt att     1359
Glu Thr Phe Lys Leu Glu Met Met Ser Ala Glu Ala Met Ile Ser Ile
        415                 420                 425

ctc cag tca agg atc gat gcg ctg cgt cag gag aac gag gaa ctc aag     1407
Leu Gln Ser Arg Ile Asp Ala Leu Arg Gln Glu Asn Glu Glu Leu Lys
    430                 435                 440

aag aac aat gct aat gga caa taa aggctctaaa aacatctctc caggttactt     1461
Lys Asn Asn Ala Asn Gly Gln
445                 450

cttattgccc ttcgcctttt atttagcttt aatctcccta atactatgac ccatctacat     1521

agctcctcta gacagattgc gaactgtgtg aatctctgtt gtaacatagg ataaaacgga     1581

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MBI-17 Sequence Listing.ST25

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            20                  25                  30

Phe His Pro Thr Asp Glu Glu Leu Val Ser Tyr Tyr Leu Lys Arg Lys
        35                  40                  45

Val Leu Gly Gln Pro Val Arg Phe Asp Ala Ile Gly Glu Val Asp Ile
    50                  55                  60

Tyr Lys His Glu Pro Trp Asp Leu Ala Val Phe Ser Arg Leu Lys Thr
65                  70                  75                  80

Arg Asp Gln Glu Trp Tyr Phe Tyr Ser Ala Leu Asp Lys Lys Tyr Gly
                85                  90                  95

Asn Gly Ala Arg Met Asn Arg Ala Thr Asn Arg Gly Tyr Trp Lys Ala
            100                 105                 110

Thr Gly Lys Asp Arg Glu Ile Arg Arg Asp Ile Leu Leu Leu Gly Met
        115                 120                 125

Lys Lys Thr Leu Val Phe His Ser Gly Arg Ala Pro Asp Gly Leu Arg
    130                 135                 140

Thr Asn Trp Val Met His Glu Tyr Arg Leu Val Glu Tyr Glu Thr Glu
145                 150                 155                 160

Lys Asn Gly Asn Leu Val Gln Asp Ala Tyr Val Leu Cys Arg Val Phe
                165                 170                 175

His Lys Asn Asn Ile Gly Pro Pro Ser Gly Asn Arg Tyr Ala Pro Phe
            180                 185                 190

Met Glu Glu Glu Trp Ala Asp Asp Glu Gly Ala Leu Ile Pro Gly Ile
        195                 200                 205

Asp Val Lys Leu Arg Leu Glu Pro Pro Pro Val Ala Asn Gly Asn Asp
    210                 215                 220

Gln Met Asp Gln Glu Ile Gln Ser Ala Ser Lys Ser Leu Ile Asn Ile
225                 230                 235                 240

Asn Glu Pro Pro Arg Glu Thr Ala Pro Leu Asp Ile Glu Ser Asp Gln
                245                 250                 255

Gln Asn His His Glu Asn Asp Leu Lys Pro Glu Glu His Asn Asn Asn
            260                 265                 270

Asn Asn Tyr Asp Glu Asn Glu Glu Thr Leu Lys Arg Glu Gln Met Glu
        275                 280                 285
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Glu Glu Glu Arg Pro Pro Arg Pro Val Cys Val Leu Asn Lys Glu Ala
290 295 300

Pro Leu Pro Leu Leu Gln Tyr Lys Arg Arg Arg Gln Ser Glu Ser Asn
305 310 315 320

Asn Asn Ser Ser Arg Asn Thr Gln Asp His Cys Ser Ser Thr Thr Thr
325 330 335

Thr Val Asp Asn Thr Thr Thr Leu Ile Ser Ser Ser Ala Ala Ala Thr
340 345 350

Asn Thr Ala Ile Ser Ala Leu Leu Glu Phe Ser Leu Met Gly Ile Ser
355 360 365

Asp Lys Lys Glu Lys Pro Gln Gln Pro Leu Arg Pro His Lys Glu Pro
370 375 380

Leu Pro Pro Gln Thr Pro Leu Ala Ser Pro Glu Glu Lys Val Asn Asp
385 390 395 400

Leu Gln Lys Glu Ile His Gln Met Ser Val Glu Arg Glu Thr Phe Lys
405 410 415

Leu Glu Met Met Ser Ala Glu Ala Met Ile Ser Ile Leu Gln Ser Arg
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Cys Val Pro Asn Cys His Ile Asp Asp Thr Pro Ala Ala Ala Thr Thr
5 10 15

acc gtc cgc tcc acc aca gcc gca gac atc ccc ata tta gac tac gag 154
Thr Val Arg Ser Thr Thr Ala Ala Asp Ile Pro Ile Leu Asp Tyr Glu
20 25 30 35

gta gcc gag ctg acg tgg gag aac ggg caa cta ggc ttg cac ggc tta 202
Val Ala Glu Leu Thr Trp Glu Asn Gly Gln Leu Gly Leu His Gly Leu
40 45 50

ggt cca ccg cga gtg acg gct tcg tcg acc aag tac tcc aca ggc gcc 250
Gly Pro Pro Arg Val Thr Ala Ser Ser Thr Lys Tyr Ser Thr Gly Ala
55 60 65

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ggt gga acg ttg gag tcg ata gtg gac caa gct act cgc ctc cct aac      298
Gly Gly Thr Leu Glu Ser Ile Val Asp Gln Ala Thr Arg Leu Pro Asn
        70                  75                  80

cct aag ccc acg gat gag ctc gtc ccg tgg ttc cat cat cgc tcc tcc      346
Pro Lys Pro Thr Asp Glu Leu Val Pro Trp Phe His His Arg Ser Ser
    85                  90                  95

agg gcc gcg atg gca atg gac gcg ctt gtc cct tgc tcc aac cta gta      394
Arg Ala Ala Met Ala Met Asp Ala Leu Val Pro Cys Ser Asn Leu Val
100                 105                 110                 115

cac gag cag cag agc aag cct ggt ggc gtt ggc tcc acc cgg gtg ggg      442
His Glu Gln Gln Ser Lys Pro Gly Gly Val Gly Ser Thr Arg Val Gly
                120                 125                 130

tca tgt agc gat ggt cgt acc atg ggc ggt gga aaa cga gca aga gtg      490
Ser Cys Ser Asp Gly Arg Thr Met Gly Gly Gly Lys Arg Ala Arg Val
            135                 140                 145

gca ccg gag tgg agc ggc ggc ggg agt cag cgg ctg acc atg gac act      538
Ala Pro Glu Trp Ser Gly Gly Gly Ser Gln Arg Leu Thr Met Asp Thr
        150                 155                 160

tac gac gta ggt ttc acc tca aca tca atg ggc tcg cac gat aac aca      586
Tyr Asp Val Gly Phe Thr Ser Thr Ser Met Gly Ser His Asp Asn Thr
    165                 170                 175

atc gac gat cat gac tcc gtc tgc cac agc cgc cca cag atg gag gac      634
Ile Asp Asp His Asp Ser Val Cys His Ser Arg Pro Gln Met Glu Asp
180                 185                 190                 195

gaa gaa gag aag aaa gcc gga gga aaa tca tca gtt tca acc aag aga      682
Glu Glu Glu Lys Lys Ala Gly Gly Lys Ser Ser Val Ser Thr Lys Arg
                200                 205                 210

agc aga gct gct gct att cat aac caa tcc gaa cgt aag agg aga gat      730
Ser Arg Ala Ala Ala Ile His Asn Gln Ser Glu Arg Lys Arg Arg Asp
            215                 220                 225

aaa atc aat caa agg atg aag act ttg caa aaa ctg gtt ccc aat tcc      778
Lys Ile Asn Gln Arg Met Lys Thr Leu Gln Lys Leu Val Pro Asn Ser
        230                 235                 240

agc aag acg gat aaa gca tct atg ttg gat gaa gtg ata gag tat ttg      826
Ser Lys Thr Asp Lys Ala Ser Met Leu Asp Glu Val Ile Glu Tyr Leu
    245                 250                 255

aag caa ctt caa gca caa gtg agc atg atg agc aga atg aat atg cct      874
Lys Gln Leu Gln Ala Gln Val Ser Met Met Ser Arg Met Asn Met Pro
260                 265                 270                 275

tct atg atg ctt cct atg gcc atg cag caa caa caa caa cta caa atg      922
Ser Met Met Leu Pro Met Ala Met Gln Gln Gln Gln Gln Leu Gln Met
                280                 285                 290

tct ctc atg tcc aat ccc atg ggt tta ggg atg ggc atg ggg atg ccc      970
Ser Leu Met Ser Asn Pro Met Gly Leu Gly Met Gly Met Gly Met Pro
            295                 300                 305

ggt ctc ggt ctc ctc gac ctt aat tct atg aac cga gct gct gca agc     1018
Gly Leu Gly Leu Leu Asp Leu Asn Ser Met Asn Arg Ala Ala Ala Ser
        310                 315                 320

gct cct aat atc cat gcc aac atg atg cca aac cca ttt ttg ccc atg     1066
Ala Pro Asn Ile His Ala Asn Met Met Pro Asn Pro Phe Leu Pro Met
    325                 330                 335

aat tgt cca tcg tgg gat gct tct tcc aat gac tct cga ttt cag tct     1114
Asn Cys Pro Ser Trp Asp Ala Ser Ser Asn Asp Ser Arg Phe Gln Ser
340                 345                 350                 355

cct ctc atc ccc gat cct atg tct gcc ttt ctt gca tgc tct act cag     1162
Pro Leu Ile Pro Asp Pro Met Ser Ala Phe Leu Ala Cys Ser Thr Gln
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360 365 370

cca acg acg atg gaa gcg tat agc agg atg gct aca tta tat cag caa 1210
Pro Thr Thr Met Glu Ala Tyr Ser Arg Met Ala Thr Leu Tyr Gln Gln
375 380 385

atg caa caa caa ctt cct cct cct tcg aat cca aaa tga ttattactca 1259
Met Gln Gln Gln Leu Pro Pro Pro Ser Asn Pro Lys
390 395

aacacctcta tatagtttac gtctatatat gtgttagtca catacataca tatatatatt 1319

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35 40 45

His Gly Leu Gly Pro Pro Arg Val Thr Ala Ser Ser Thr Lys Tyr Ser
50 55 60

Thr Gly Ala Gly Gly Thr Leu Glu Ser Ile Val Asp Gln Ala Thr Arg
65 70 75 80

Leu Pro Asn Pro Lys Pro Thr Asp Glu Leu Val Pro Trp Phe His His
85 90 95

Arg Ser Ser Arg Ala Ala Met Ala Met Asp Ala Leu Val Pro Cys Ser
100 105 110

Asn Leu Val His Glu Gln Gln Ser Lys Pro Gly Gly Val Gly Ser Thr
115 120 125

Arg Val Gly Ser Cys Ser Asp Gly Arg Thr Met Gly Gly Gly Lys Arg
130 135 140

Ala Arg Val Ala Pro Glu Trp Ser Gly Gly Gly Ser Gln Arg Leu Thr
145 150 155 160

Met Asp Thr Tyr Asp Val Gly Phe Thr Ser Thr Ser Met Gly Ser His
165 170 175

Asp Asn Thr Ile Asp Asp His Asp Ser Val Cys His Ser Arg Pro Gln
180 185 190

Met Glu Asp Glu Glu Glu Lys Lys Ala Gly Gly Lys Ser Ser Val Ser
195 200 205

Thr Lys Arg Ser Arg Ala Ala Ala Ile His Asn Gln Ser Glu Arg Lys
210 215 220

Arg Arg Asp Lys Ile Asn Gln Arg Met Lys Thr Leu Gln Lys Leu Val
225 230 235 240

Pro Asn Ser Ser Lys Thr Asp Lys Ala Ser Met Leu Asp Glu Val Ile
245 250 255

Glu Tyr Leu Lys Gln Leu Gln Ala Gln Val Ser Met Met Ser Arg Met
260 265 270

Asn Met Pro Ser Met Met Leu Pro Met Ala Met Gln Gln Gln Gln Gln
275 280 285

Leu Gln Met Ser Leu Met Ser Asn Pro Met Gly Leu Gly Met Gly Met
290 295 300

Gly Met Pro Gly Leu Gly Leu Leu Asp Leu Asn Ser Met Asn Arg Ala
305 310 315 320

Ala Ala Ser Ala Pro Asn Ile His Ala Asn Met Met Pro Asn Pro Phe
325 330 335

Leu Pro Met Asn Cys Pro Ser Trp Asp Ala Ser Ser Asn Asp Ser Arg
340 345 350

Phe Gln Ser Pro Leu Ile Pro Asp Pro Met Ser Ala Phe Leu Ala Cys
355 360 365

Ser Thr Gln Pro Thr Thr Met Glu Ala Tyr Ser Arg Met Ala Thr Leu
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Tyr Gln Gln Met Gln Gln Gln Leu Pro Pro Pro Ser Asn Pro Lys
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ttgtaaaagt ggatcggagg tatggaaagg gaccggttcc accggaaaca tcggcggcgg 240

cggatgataa ttcgtcttgg aacgagactg atgtcaccgc c atg gtc tcc gct ctc 296
Met Val Ser Ala Leu
1 5

agc cgt gtc ata gag aat ccg aca gac ccg ccg gtc aaa caa gag ctt 344
Ser Arg Val Ile Glu Asn Pro Thr Asp Pro Pro Val Lys Gln Glu Leu

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gat aaa tcg gat caa cat caa cca gac caa gat caa cca aga aga aga      392
Asp Lys Ser Asp Gln His Gln Pro Asp Gln Asp Gln Pro Arg Arg Arg
            25                  30                  35

cac tat aga ggc gta agg cag aga cca tgg ggt aaa tgg gcg gca gaa      440
His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu
        40                  45                  50

atc cgc gat cca aag aaa gca gcc cgt gtc tgg ctc ggg act ttc gag      488
Ile Arg Asp Pro Lys Lys Ala Ala Arg Val Trp Leu Gly Thr Phe Glu
    55                  60                  65

acg gca gag gaa gct gct tta gcc tat gac cga gct gcc ctc aaa ttc      536
Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Arg Ala Ala Leu Lys Phe
70                  75                  80                  85

aaa ggc acc aag gct aaa ctg aac ttc cct gaa cgg gtc caa ggc cct      584
Lys Gly Thr Lys Ala Lys Leu Asn Phe Pro Glu Arg Val Gln Gly Pro
                90                  95                  100

act acc acc aca acc att tct cat gca cca aga gga gtt agt gaa tcc      632
Thr Thr Thr Thr Thr Ile Ser His Ala Pro Arg Gly Val Ser Glu Ser
            105                 110                 115

atg aac tca cct cct cct cga cct ggt cca cct tca act act act act      680
Met Asn Ser Pro Pro Pro Arg Pro Gly Pro Pro Ser Thr Thr Thr Thr
        120                 125                 130

tcg tgg cca atg act tat aac cag gac ata ctt caa tac gct cag ttg      728
Ser Trp Pro Met Thr Tyr Asn Gln Asp Ile Leu Gln Tyr Ala Gln Leu
    135                 140                 145

ctt acg agt aac aat gag gtt gat tta tca tac tac acg tcg act ctc      776
Leu Thr Ser Asn Asn Glu Val Asp Leu Ser Tyr Tyr Thr Ser Thr Leu
150                 155                 160                 165

ttc agt caa cct ttt tca acg cct tct tca tct tct tct tcc tcc caa      824
Phe Ser Gln Pro Phe Ser Thr Pro Ser Ser Ser Ser Ser Ser Ser Gln
                170                 175                 180

cag acg cag caa cag cag cta caa caa caa caa cag cag cgt gaa gaa      872
Gln Thr Gln Gln Gln Gln Leu Gln Gln Gln Gln Gln Gln Arg Glu Glu
            185                 190                 195

gaa gag aag aat tat ggt tac aat tat tat aac tac cca aga gaa taa      920
Glu Glu Lys Asn Tyr Gly Tyr Asn Tyr Tyr Asn Tyr Pro Arg Glu
        200                 205                 210

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Gln Pro Arg Arg Arg His Tyr Arg Gly Val Arg Gln Arg Pro Trp Gly
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35 40 45

Lys Trp Ala Ala Glu Ile Arg Asp Pro Lys Lys Ala Ala Arg Val Trp
50 55 60

Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Arg
65 70 75 80

Ala Ala Leu Lys Phe Lys Gly Thr Lys Ala Lys Leu Asn Phe Pro Glu
85 90 95

Arg Val Gln Gly Pro Thr Thr Thr Thr Thr Ile Ser His Ala Pro Arg
100 105 110

Gly Val Ser Glu Ser Met Asn Ser Pro Pro Pro Arg Pro Gly Pro Pro
115 120 125

Ser Thr Thr Thr Thr Ser Trp Pro Met Thr Tyr Asn Gln Asp Ile Leu
130 135 140

Gln Tyr Ala Gln Leu Leu Thr Ser Asn Asn Glu Val Asp Leu Ser Tyr
145 150 155 160

Tyr Thr Ser Thr Leu Phe Ser Gln Pro Phe Ser Thr Pro Ser Ser Ser
165 170 175

Ser Ser Ser Ser Gln Gln Thr Gln Gln Gln Gln Leu Gln Gln Gln Gln
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Gln Gln Arg Glu Glu Glu Glu Lys Asn Tyr Gly Tyr Asn Tyr Tyr Asn
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Tyr Pro Arg Glu
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ctccgatttc atcatcatct tccccatcat cgtcgtcttt gaaatcttgt cttctcaacg 180

ctcttcactt ctgctgtaat aagcagaggc ttgttctgga gactccttct ctttccatgc 240

gcttaagacc caaaaggact tgttctagtg ttgaagtctt tgggggtttt cacataaagc 300

agcaaaagtt ttctttttttc atagttcgct gagagttttg agttttgata ccaaaaaagt 360

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Met Val Ala Ile Arg Lys Glu Gln Ser Leu Ser Gly Val Ser

MBI-17 Sequence Listing.ST25

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15                  20                  25                  30

caa gaa acc caa cct ttg agg aaa gtc cgt att att gtg aat gat cct      565
Gln Glu Thr Gln Pro Leu Arg Lys Val Arg Ile Ile Val Asn Asp Pro
                35                  40                  45

tat gct act gat gat tcc tct agt gat gag gaa gag ctt aag gtt cct      613
Tyr Ala Thr Asp Asp Ser Ser Ser Asp Glu Glu Glu Leu Lys Val Pro
            50                  55                  60

aag cca agg aaa atg aaa cgt atc gtt cgt gag att aac ttt cct tct      661
Lys Pro Arg Lys Met Lys Arg Ile Val Arg Glu Ile Asn Phe Pro Ser
        65                  70                  75

atg gaa gtt tct gaa cag cct tct gag agt tct tct cag gac agt act      709
Met Glu Val Ser Glu Gln Pro Ser Glu Ser Ser Ser Gln Asp Ser Thr
    80                  85                  90

aaa act gat ggc aag ata gct gtg tca gct tct cct gct gtt cct agg      757
Lys Thr Asp Gly Lys Ile Ala Val Ser Ala Ser Pro Ala Val Pro Arg
95                  100                 105                 110

aag aag cct gtt ggt gtt agg caa agg aaa tgg ggg aaa tgg gct gct      805
Lys Lys Pro Val Gly Val Arg Gln Arg Lys Trp Gly Lys Trp Ala Ala
                115                 120                 125

gag att aga gat cct att aag aaa act agg act tgg ttg ggt act ttt      853
Glu Ile Arg Asp Pro Ile Lys Lys Thr Arg Thr Trp Leu Gly Thr Phe
            130                 135                 140

gat act ctt gaa gaa gct gct aaa gct tat gat gct aag aag ctt gag      901
Asp Thr Leu Glu Glu Ala Ala Lys Ala Tyr Asp Ala Lys Lys Leu Glu
        145                 150                 155

ttt gat gct att gtt gct gga aat gtg tcc act act aaa cgt gat gtt      949
Phe Asp Ala Ile Val Ala Gly Asn Val Ser Thr Thr Lys Arg Asp Val
    160                 165                 170

tct tca tct gag act agc caa tgc tct cgt tct tca cct gtt gtt cct      997
Ser Ser Ser Glu Thr Ser Gln Cys Ser Arg Ser Ser Pro Val Val Pro
175                 180                 185                 190

gtt gag caa gat gac act tct gca tca gct ctc act tgt gtc aac aac     1045
Val Glu Gln Asp Asp Thr Ser Ala Ser Ala Leu Thr Cys Val Asn Asn
                195                 200                 205

cct gat gac gtc tcg acc gtt gct cca act gct cca act cca aat gtt     1093
Pro Asp Asp Val Ser Thr Val Ala Pro Thr Ala Pro Thr Pro Asn Val
            210                 215                 220

cct gct ggt gga aac aag gaa acg ttg ttc gat ttc gac ttt act aat     1141
Pro Ala Gly Gly Asn Lys Glu Thr Leu Phe Asp Phe Asp Phe Thr Asn
        225                 230                 235

cta cag atc cct gat ttt ggt ttc ttg gca gag gag caa caa gac cta     1189
Leu Gln Ile Pro Asp Phe Gly Phe Leu Ala Glu Glu Gln Gln Asp Leu
    240                 245                 250

gac ttc gat tgt ttc ctc gcg gat gat cag ttt gat gat ttc ggc ttg     1237
Asp Phe Asp Cys Phe Leu Ala Asp Asp Gln Phe Asp Asp Phe Gly Leu
255                 260                 265                 270

ctt gat gac att caa gga ttc gaa gat aac ggt cca agt gcg tta cca     1285
Leu Asp Asp Ile Gln Gly Phe Glu Asp Asn Gly Pro Ser Ala Leu Pro
                275                 280                 285

gat ttc gac ttt gcg gat gtt gaa gat ctt cag cta gct gac tct agt     1333
Asp Phe Asp Phe Ala Asp Val Glu Asp Leu Gln Leu Ala Asp Ser Ser
            290                 295                 300

ttc ggt ttc ctt gat caa ctt gct cct atc aac atc tct tgc cca tta     1381
```

Phe Gly Phe Leu Asp Gln Leu Ala Pro Ile Asn Ile Ser Cys Pro Leu
305 310 315

aaa agt ttt gca gct tca tag gatcttgctt agtaatgtta agtgagaaga 1432
Lys Ser Phe Ala Ala Ser
320

gtgttttgtt ttttcgttta tgctttagta atttaagaca tacaaaagtg tgtgttccgg 1492

attgtagtaa gatcttaaga cataaagccg ggttttgcaa ttaggaatcg agttttaatg 1552

aagttttagt ttatgtttg 1571

<210> 20
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<212> PRT
<213> Arabidopsis thaliana

<400> 20

Met Val Ala Ile Arg Lys Glu Gln Ser Leu Ser Gly Val Ser Ser Glu
1 5 10 15

Ile Lys Lys Arg Ala Lys Arg Asn Thr Leu Ser Ser Leu Pro Gln Glu
20 25 30

Thr Gln Pro Leu Arg Lys Val Arg Ile Ile Val Asn Asp Pro Tyr Ala
35 40 45

Thr Asp Asp Ser Ser Ser Asp Glu Glu Glu Leu Lys Val Pro Lys Pro
50 55 60

Arg Lys Met Lys Arg Ile Val Arg Glu Ile Asn Phe Pro Ser Met Glu
65 70 75 80

Val Ser Glu Gln Pro Ser Glu Ser Ser Ser Gln Asp Ser Thr Lys Thr
85 90 95

Asp Gly Lys Ile Ala Val Ser Ala Ser Pro Ala Val Pro Arg Lys Lys
100 105 110

Pro Val Gly Val Arg Gln Arg Lys Trp Gly Lys Trp Ala Ala Glu Ile
115 120 125

Arg Asp Pro Ile Lys Lys Thr Arg Thr Trp Leu Gly Thr Phe Asp Thr
130 135 140

Leu Glu Glu Ala Ala Lys Ala Tyr Asp Ala Lys Lys Leu Glu Phe Asp
145 150 155 160

Ala Ile Val Ala Gly Asn Val Ser Thr Thr Lys Arg Asp Val Ser Ser
165 170 175

Ser Glu Thr Ser Gln Cys Ser Arg Ser Ser Pro Val Val Pro Val Glu
180 185 190

Gln Asp Asp Thr Ser Ala Ser Ala Leu Thr Cys Val Asn Asn Pro Asp
195 200 205

Asp Val Ser Thr Val Ala Pro Thr Ala Pro Thr Pro Asn Val Pro Ala
210 215 220

```
Gly Gly Asn Lys Glu Thr Leu Phe Asp Phe Asp Phe Thr Asn Leu Gln
225                 230                 235                 240

Ile Pro Asp Phe Gly Phe Leu Ala Glu Glu Gln Gln Asp Leu Asp Phe
                245                 250                 255

Asp Cys Phe Leu Ala Asp Asp Gln Phe Asp Asp Phe Gly Leu Leu Asp
            260                 265                 270

Asp Ile Gln Gly Phe Glu Asp Asn Gly Pro Ser Ala Leu Pro Asp Phe
        275                 280                 285

Asp Phe Ala Asp Val Glu Asp Leu Gln Leu Ala Asp Ser Ser Phe Gly
    290                 295                 300

Phe Leu Asp Gln Leu Ala Pro Ile Asn Ile Ser Cys Pro Leu Lys Ser
305                 310                 315                 320

Phe Ala Ala Ser
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<210> 21
<211> 1195
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (67)..(1041)
<223> G883

<400> 21

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ctctctcgtc ttcgtcttct tcttcttcaa cgttcctctc caaaatcctc agaccaagaa     60

atcatc atg gcc gtc gat cta atg cgt ttc cct aag ata gat gat caa        108
       Met Ala Val Asp Leu Met Arg Phe Pro Lys Ile Asp Asp Gln
       1               5                   10

acg gct att cag gaa gct gca tcg caa ggt tta caa agt atg gaa cat      156
Thr Ala Ile Gln Glu Ala Ala Ser Gln Gly Leu Gln Ser Met Glu His
15                  20                  25                  30

ctg atc cgt gtc ctc tct aac cgt ccc gaa caa caa cac aac gtt gac      204
Leu Ile Arg Val Leu Ser Asn Arg Pro Glu Gln Gln His Asn Val Asp
                35                  40                  45

tgc tcc gag atc act gac ttc acc gtt tct aaa ttc aaa acc gtc att      252
Cys Ser Glu Ile Thr Asp Phe Thr Val Ser Lys Phe Lys Thr Val Ile
            50                  55                  60

tct ctc ctt aac cgt act ggt cac gct cgg ttc aga cgc gga ccg gtt      300
Ser Leu Leu Asn Arg Thr Gly His Ala Arg Phe Arg Arg Gly Pro Val
        65                  70                  75

cac tcc act tcc tct gcc gca tct cag aaa cta cag agt cag atc gtt      348
His Ser Thr Ser Ser Ala Ala Ser Gln Lys Leu Gln Ser Gln Ile Val
    80                  85                  90

aaa aat act caa cct gag gct ccg ata gtg aga aca act acg aat cac      396
Lys Asn Thr Gln Pro Glu Ala Pro Ile Val Arg Thr Thr Thr Asn His
95                  100                 105                 110

cct caa atc gtt cct cca ccg tct agt gta aca ctc gat ttc tct aaa      444
Pro Gln Ile Val Pro Pro Pro Ser Ser Val Thr Leu Asp Phe Ser Lys
                115                 120                 125
```

```
cca agc atc ttc ggc acc aaa gct aag agc gcc gag ctg gaa ttc tcc      492
Pro Ser Ile Phe Gly Thr Lys Ala Lys Ser Ala Glu Leu Glu Phe Ser
            130                 135                 140

aaa gaa aac ttc agt gtt tct tta aac tcc tca ttc atg tcg tcg gcg      540
Lys Glu Asn Phe Ser Val Ser Leu Asn Ser Ser Phe Met Ser Ser Ala
        145                 150                 155

ata acc gga gac ggc agc gtc tcc aat gga aaa atc ttc ctt gct tct      588
Ile Thr Gly Asp Gly Ser Val Ser Asn Gly Lys Ile Phe Leu Ala Ser
    160                 165                 170

gct ccg tcg cag cct gtt aac tct tcc gga aaa cca ccg ttg gct ggt      636
Ala Pro Ser Gln Pro Val Asn Ser Ser Gly Lys Pro Pro Leu Ala Gly
175                 180                 185                 190

cat cct tac aga aag aga tgt ctc gag cat gag cac tca gag agt ttc      684
His Pro Tyr Arg Lys Arg Cys Leu Glu His Glu His Ser Glu Ser Phe
                195                 200                 205

tcc gga aaa gtc tcc ggc tcc gcc tac gga aag tgc cat tgc aag aaa      732
Ser Gly Lys Val Ser Gly Ser Ala Tyr Gly Lys Cys His Cys Lys Lys
            210                 215                 220

agg aaa aat cgg atg aag aga acc gtg aga gta ccg gcg ata agt gca      780
Arg Lys Asn Arg Met Lys Arg Thr Val Arg Val Pro Ala Ile Ser Ala
        225                 230                 235

aag atc gcc gat att cca ccg gac gaa tat tcg tgg agg aag tac gga      828
Lys Ile Ala Asp Ile Pro Pro Asp Glu Tyr Ser Trp Arg Lys Tyr Gly
    240                 245                 250

caa aaa ccg atc aag ggc tca cca cac cca cgt ggt tac tac aag tgc      876
Gln Lys Pro Ile Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr Lys Cys
255                 260                 265                 270

agt aca ttc aga gga tgt cca gcg agg aaa cac gtg gaa cga gca tta      924
Ser Thr Phe Arg Gly Cys Pro Ala Arg Lys His Val Glu Arg Ala Leu
                275                 280                 285

gat gat cca gcg atg ctt att gtg aca tac gaa gga gag cac cgt cat      972
Asp Asp Pro Ala Met Leu Ile Val Thr Tyr Glu Gly Glu His Arg His
            290                 295                 300

aac caa tcc gcg atg cag gag aat att tct tct tca ggc att aat gat     1020
Asn Gln Ser Ala Met Gln Glu Asn Ile Ser Ser Ser Gly Ile Asn Asp
        305                 310                 315

tta gtg ttt gcc tcg gct tga ctttttttg tactatttgt tttttgattt         1071
Leu Val Phe Ala Ser Ala
    320

tttgagtact ttagatggat tgaaatttgt aaatttttt attaagaaat caatttaaat    1131

agagaaaaat tagtggtggt gcaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa   1191

aaaa                                                                1195


<210>  22
<211>  324
<212>  PRT
<213>  Arabidopsis thaliana

<400>  22

Met Ala Val Asp Leu Met Arg Phe Pro Lys Ile Asp Asp Gln Thr Ala
1               5                   10                  15


Ile Gln Glu Ala Ala Ser Gln Gly Leu Gln Ser Met Glu His Leu Ile
            20                  25                  30
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```
Arg Val Leu Ser Asn Arg Pro Glu Gln Gln His Asn Val Asp Cys Ser
        35                  40                  45

Glu Ile Thr Asp Phe Thr Val Ser Lys Phe Lys Thr Val Ile Ser Leu
    50                  55                  60

Leu Asn Arg Thr Gly His Ala Arg Phe Arg Arg Gly Pro Val His Ser
65                  70                  75                  80

Thr Ser Ser Ala Ala Ser Gln Lys Leu Gln Ser Gln Ile Val Lys Asn
                85                  90                  95

Thr Gln Pro Glu Ala Pro Ile Val Arg Thr Thr Thr Asn His Pro Gln
            100                 105                 110

Ile Val Pro Pro Pro Ser Ser Val Thr Leu Asp Phe Ser Lys Pro Ser
        115                 120                 125

Ile Phe Gly Thr Lys Ala Lys Ser Ala Glu Leu Glu Phe Ser Lys Glu
    130                 135                 140

Asn Phe Ser Val Ser Leu Asn Ser Ser Phe Met Ser Ser Ala Ile Thr
145                 150                 155                 160

Gly Asp Gly Ser Val Ser Asn Gly Lys Ile Phe Leu Ala Ser Ala Pro
                165                 170                 175

Ser Gln Pro Val Asn Ser Ser Gly Lys Pro Pro Leu Ala Gly His Pro
            180                 185                 190

Tyr Arg Lys Arg Cys Leu Glu His Glu His Ser Glu Ser Phe Ser Gly
        195                 200                 205

Lys Val Ser Gly Ser Ala Tyr Gly Lys Cys His Cys Lys Lys Arg Lys
    210                 215                 220

Asn Arg Met Lys Arg Thr Val Arg Val Pro Ala Ile Ser Ala Lys Ile
225                 230                 235                 240

Ala Asp Ile Pro Pro Asp Glu Tyr Ser Trp Arg Lys Tyr Gly Gln Lys
                245                 250                 255

Pro Ile Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr Lys Cys Ser Thr
            260                 265                 270

Phe Arg Gly Cys Pro Ala Arg Lys His Val Glu Arg Ala Leu Asp Asp
        275                 280                 285

Pro Ala Met Leu Ile Val Thr Tyr Glu Gly Glu His Arg His Asn Gln
    290                 295                 300

Ser Ala Met Gln Glu Asn Ile Ser Ser Ser Gly Ile Asn Asp Leu Val
305                 310                 315                 320

Phe Ala Ser Ala
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<210> 23
<211> 1755
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(1755)
<223> G938

<400> 23

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atg atg atg ttt aac gag atg gga atg tat gga aac atg gat ttc ttc       48
Met Met Met Phe Asn Glu Met Gly Met Tyr Gly Asn Met Asp Phe Phe
1               5                  10                  15

tct tcc tcc aca tct ctc gat gtg tgt cca tta cca caa gct gaa caa       96
Ser Ser Ser Thr Ser Leu Asp Val Cys Pro Leu Pro Gln Ala Glu Gln
            20                  25                  30

gaa cct gta gtt gaa gat gtc gac tac acc gat gat gag atg gat gtg      144
Glu Pro Val Val Glu Asp Val Asp Tyr Thr Asp Asp Glu Met Asp Val
        35                  40                  45

gat gag ctt gag aag agg atg tgg aga gac aaa atg cgt ttg aaa cgt      192
Asp Glu Leu Glu Lys Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
    50                  55                  60

ctc aag gag caa cag agt aag tgt aaa gaa ggc gtc gat ggt tcg aaa      240
Leu Lys Glu Gln Gln Ser Lys Cys Lys Glu Gly Val Asp Gly Ser Lys
65                  70                  75                  80

cag agg cag tcg caa gag caa gct agg agg aag aaa atg tct aga gcc      288
Gln Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala
                85                  90                  95

caa gat ggg atc ttg aag tat atg ttg aag atg atg gaa gtt tgt aaa      336
Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys
            100                 105                 110

gct caa ggc ttt gtt tat ggt att att cct gag aag ggt aag cct gtg      384
Ala Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Lys Gly Lys Pro Val
        115                 120                 125

act ggt gct tcg gat aat ttg agg gaa tgg tgg aaa gat aag gtt agg      432
Thr Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg
    130                 135                 140

ttt gat cgt aat ggt cca gct gct att gct aag tat cag tca gag aat      480
Phe Asp Arg Asn Gly Pro Ala Ala Ile Ala Lys Tyr Gln Ser Glu Asn
145                 150                 155                 160

aat att tct gga ggg agt aat gat tgt aac agc ttg gtt ggt cca aca      528
Asn Ile Ser Gly Gly Ser Asn Asp Cys Asn Ser Leu Val Gly Pro Thr
                165                 170                 175

ccg cat acg ctt cag gag ctt cag gac acg act ctt ggt tcg ctt tta      576
Pro His Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu
            180                 185                 190

tcg gct ttg atg caa cat tgt gat cca ccg cag aga cgg ttt cct ttg      624
Ser Ala Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu
        195                 200                 205

gag aaa gga gtt tct cca cct tgg tgg cct aat ggg aat gaa gag tgg      672
Glu Lys Gly Val Ser Pro Pro Trp Trp Pro Asn Gly Asn Glu Glu Trp
    210                 215                 220

tgg cct cag ctt ggt tta cca aat gag caa ggt cct cct cct tat aag      720
Trp Pro Gln Leu Gly Leu Pro Asn Glu Gln Gly Pro Pro Pro Tyr Lys
225                 230                 235                 240

aag cct cat gat ttg aag aaa gct tgg aaa gtc ggt gtt tta act gcg      768
Lys Pro His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala
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                245                 250                 255

gtg atc aag cat atg tcg ccg gat att gcg aag atc cgt aag ctt gtg      816
Val Ile Lys His Met Ser Pro Asp Ile Ala Lys Ile Arg Lys Leu Val
            260                 265                 270

agg caa tca aaa tgc ttg cag gat aag atg acg gcg aaa gag agt gct      864
Arg Gln Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala
        275                 280                 285

act tgg ctt gcc att att aac caa gaa gag gtt gtg gct cgg gag ctt      912
Thr Trp Leu Ala Ile Ile Asn Gln Glu Glu Val Val Ala Arg Glu Leu
    290                 295                 300

tat ccc gag tca tgc cct cct ctt tct tct tct tca tca tta gga agc      960
Tyr Pro Glu Ser Cys Pro Pro Leu Ser Ser Ser Ser Ser Leu Gly Ser
305                 310                 315                 320

ggg tcg ctt ctc att aat gat tgt agc gag tat gac gtt gaa ggt ttc     1008
Gly Ser Leu Leu Ile Asn Asp Cys Ser Glu Tyr Asp Val Glu Gly Phe
                325                 330                 335

gag aag gaa caa cat ggt ttc gat gtg gaa gag cgg aaa cca gag ata     1056
Glu Lys Glu Gln His Gly Phe Asp Val Glu Glu Arg Lys Pro Glu Ile
            340                 345                 350

gtg atg atg cat cct cta gca agc ttt ggg gtt gct aaa atg caa cat     1104
Val Met Met His Pro Leu Ala Ser Phe Gly Val Ala Lys Met Gln His
        355                 360                 365

ttt ccc ata aag gag gag gtc gcc acc acg gta aac tta gag ttc acg     1152
Phe Pro Ile Lys Glu Glu Val Ala Thr Thr Val Asn Leu Glu Phe Thr
    370                 375                 380

aga aag agg aag cag aac aat gat atg aat gtt atg gta atg gac aga     1200
Arg Lys Arg Lys Gln Asn Asn Asp Met Asn Val Met Val Met Asp Arg
385                 390                 395                 400

tca gca ggt tac act tgt gag aat ggt cag tgt cct cac agc aaa atg     1248
Ser Ala Gly Tyr Thr Cys Glu Asn Gly Gln Cys Pro His Ser Lys Met
                405                 410                 415

aat ctt gga ttt caa gac agg agt tca agg gac aac cac cag atg gtt     1296
Asn Leu Gly Phe Gln Asp Arg Ser Ser Arg Asp Asn His Gln Met Val
            420                 425                 430

tgt cca tat aga gac aat cgt tta gcg tat gga gca tcc aag ttt cat     1344
Cys Pro Tyr Arg Asp Asn Arg Leu Ala Tyr Gly Ala Ser Lys Phe His
        435                 440                 445

atg ggt gga atg aaa cta gta gtt cct cag caa cca gtc caa ccg atc     1392
Met Gly Gly Met Lys Leu Val Val Pro Gln Gln Pro Val Gln Pro Ile
    450                 455                 460

gac cta tcg ggc gtt gga gtt ccg gaa aac ggg cag aag atg atc acc     1440
Asp Leu Ser Gly Val Gly Val Pro Glu Asn Gly Gln Lys Met Ile Thr
465                 470                 475                 480

gag ctt atg gcc atg tac gac aga aat gtc caa agc aac caa acg cct     1488
Glu Leu Met Ala Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Pro
                485                 490                 495

cct act ttg atg gaa aac caa agc atg gtc att gat gca aaa gca gct     1536
Pro Thr Leu Met Glu Asn Gln Ser Met Val Ile Asp Ala Lys Ala Ala
            500                 505                 510

cag aat cag cag ctg aat ttc aac agt ggc aat caa atg ttt atg caa     1584
Gln Asn Gln Gln Leu Asn Phe Asn Ser Gly Asn Gln Met Phe Met Gln
        515                 520                 525

caa ggg acg aac aac ggg gtt aac aat cgg ttc cag atg gtg ttt gat     1632
Gln Gly Thr Asn Asn Gly Val Asn Asn Arg Phe Gln Met Val Phe Asp
    530                 535                 540

tcg aca cca ttc gat atg gca gca ttc gat tac aga gat gat tgg caa     1680
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Ser Thr Pro Phe Asp Met Ala Ala Phe Asp Tyr Arg Asp Asp Trp Gln
545                 550                 555                 560

acc gga gca atg gaa gga atg ggg aag cag cag cag cag cag cag cag     1728
Thr Gly Ala Met Glu Gly Met Gly Lys Gln Gln Gln Gln Gln Gln Gln
                565                 570                 575

cag caa gat gta tca ata tgg ttc tga                                 1755
Gln Gln Asp Val Ser Ile Trp Phe
            580
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<210> 24
<211> 584
<212> PRT
<213> Arabidopsis thaliana

<400> 24

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Met Met Met Phe Asn Glu Met Gly Met Tyr Gly Asn Met Asp Phe Phe
1               5                   10                  15

Ser Ser Ser Thr Ser Leu Asp Val Cys Pro Leu Pro Gln Ala Glu Gln
            20                  25                  30

Glu Pro Val Val Glu Asp Val Asp Tyr Thr Asp Asp Glu Met Asp Val
        35                  40                  45

Asp Glu Leu Glu Lys Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
    50                  55                  60

Leu Lys Glu Gln Gln Ser Lys Cys Lys Glu Gly Val Asp Gly Ser Lys
65                  70                  75                  80

Gln Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala
                85                  90                  95

Gln Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys
            100                 105                 110

Ala Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Lys Gly Lys Pro Val
        115                 120                 125

Thr Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg
    130                 135                 140

Phe Asp Arg Asn Gly Pro Ala Ala Ile Ala Lys Tyr Gln Ser Glu Asn
145                 150                 155                 160

Asn Ile Ser Gly Gly Ser Asn Asp Cys Asn Ser Leu Val Gly Pro Thr
                165                 170                 175

Pro His Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu
            180                 185                 190

Ser Ala Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu
        195                 200                 205

Glu Lys Gly Val Ser Pro Pro Trp Trp Pro Asn Gly Asn Glu Glu Trp
    210                 215                 220
```

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Trp Pro Gln Leu Gly Leu Pro Asn Glu Gln Gly Pro Pro Pro Tyr Lys
225                 230                 235                 240

Lys Pro His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala
                245                 250                 255

Val Ile Lys His Met Ser Pro Asp Ile Ala Lys Ile Arg Lys Leu Val
            260                 265                 270

Arg Gln Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala
        275                 280                 285

Thr Trp Leu Ala Ile Ile Asn Gln Glu Glu Val Val Ala Arg Glu Leu
    290                 295                 300

Tyr Pro Glu Ser Cys Pro Pro Leu Ser Ser Ser Ser Ser Leu Gly Ser
305                 310                 315                 320

Gly Ser Leu Leu Ile Asn Asp Cys Ser Glu Tyr Asp Val Glu Gly Phe
                325                 330                 335

Glu Lys Glu Gln His Gly Phe Asp Val Glu Glu Arg Lys Pro Glu Ile
            340                 345                 350

Val Met Met His Pro Leu Ala Ser Phe Gly Val Ala Lys Met Gln His
        355                 360                 365

Phe Pro Ile Lys Glu Glu Val Ala Thr Thr Val Asn Leu Glu Phe Thr
    370                 375                 380

Arg Lys Arg Lys Gln Asn Asn Asp Met Asn Val Met Val Met Asp Arg
385                 390                 395                 400

Ser Ala Gly Tyr Thr Cys Glu Asn Gly Gln Cys Pro His Ser Lys Met
                405                 410                 415

Asn Leu Gly Phe Gln Asp Arg Ser Ser Arg Asp Asn His Gln Met Val
            420                 425                 430

Cys Pro Tyr Arg Asp Asn Arg Leu Ala Tyr Gly Ala Ser Lys Phe His
        435                 440                 445

Met Gly Gly Met Lys Leu Val Val Pro Gln Gln Pro Val Gln Pro Ile
    450                 455                 460

Asp Leu Ser Gly Val Gly Val Pro Glu Asn Gly Gln Lys Met Ile Thr
465                 470                 475                 480

Glu Leu Met Ala Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Pro
                485                 490                 495

Pro Thr Leu Met Glu Asn Gln Ser Met Val Ile Asp Ala Lys Ala Ala
            500                 505                 510

Gln Asn Gln Gln Leu Asn Phe Asn Ser Gly Asn Gln Met Phe Met Gln
        515                 520                 525
```

```
Gln Gly Thr Asn Asn Gly Val Asn Asn Arg Phe Gln Met Val Phe Asp
    530                 535                 540

Ser Thr Pro Phe Asp Met Ala Ala Phe Asp Tyr Arg Asp Asp Trp Gln
545                 550                 555                 560

Thr Gly Ala Met Glu Gly Met Gly Lys Gln Gln Gln Gln Gln Gln Gln
                565                 570                 575

Gln Gln Asp Val Ser Ile Trp Phe
            580
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<210> 25
<211> 1161
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (67)..(1041)
<223> G1328

<400> 25

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aattcaatca ctatattttt ttaaaaacat ttgacttcat cgatcggtta acaattaatc     60

aaaaag atg gga cga tca cca tgt tgt gag aag aag aat ggt ctc aag       108
       Met Gly Arg Ser Pro Cys Cys Glu Lys Lys Asn Gly Leu Lys
       1               5                   10

aaa gga cca tgg act cct gag gag gat caa aag ctc att gat tat atc      156
Lys Gly Pro Trp Thr Pro Glu Glu Asp Gln Lys Leu Ile Asp Tyr Ile
15                  20                  25                  30

aat ata cat ggt tat gga aat tgg aga act ctt ccc aag aat gct ggg      204
Asn Ile His Gly Tyr Gly Asn Trp Arg Thr Leu Pro Lys Asn Ala Gly
                35                  40                  45

tta caa aga tgt ggt aag agt tgt cgt ctc cgg tgg acc aac tat ctc      252
Leu Gln Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu
            50                  55                  60

cga cca gat att aag cgt gga aga ttc tct ttt gaa gaa gaa gaa acc      300
Arg Pro Asp Ile Lys Arg Gly Arg Phe Ser Phe Glu Glu Glu Glu Thr
        65                  70                  75

att att caa ctt cac agc atc atg gga aac aag tgg tct gcg att gcg      348
Ile Ile Gln Leu His Ser Ile Met Gly Asn Lys Trp Ser Ala Ile Ala
    80                  85                  90

gct cgt ttg cct gga aga aca gac aac gag atc aaa aac tat tgg aac      396
Ala Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn
95                  100                 105                 110

act cac atc aga aaa aga ctt cta aag atg gga atc gac ccg gtt aca      444
Thr His Ile Arg Lys Arg Leu Leu Lys Met Gly Ile Asp Pro Val Thr
                115                 120                 125

cac act cca cgt ctt gat ctt ctc gat atc tcc tcc att ctc agc tca      492
His Thr Pro Arg Leu Asp Leu Leu Asp Ile Ser Ser Ile Leu Ser Ser
            130                 135                 140

tct atc tac aac tct tcg cat cat cat cat cat cat cat caa caa cat      540
Ser Ile Tyr Asn Ser Ser His His His His His His His Gln Gln His
        145                 150                 155

atg aac atg tcg agg ctc atg atg agt gat ggt aat cat caa cca ttg      588
Met Asn Met Ser Arg Leu Met Met Ser Asp Gly Asn His Gln Pro Leu
    160                 165                 170
```

```
gtt aac ccc gag ata ctc aaa ctc gca acc tct ctc ttt tca aac caa      636
Val Asn Pro Glu Ile Leu Lys Leu Ala Thr Ser Leu Phe Ser Asn Gln
175                 180                 185                 190

aac cac ccc aac aac aca cac gag aac aac acg gtt aac caa acc gaa      684
Asn His Pro Asn Asn Thr His Glu Asn Asn Thr Val Asn Gln Thr Glu
                195                 200                 205

gta aac caa tac caa acc ggt tac aac atg cct ggt aat gaa gaa tta      732
Val Asn Gln Tyr Gln Thr Gly Tyr Asn Met Pro Gly Asn Glu Glu Leu
            210                 215                 220

caa tct tgg ttc cct atc atg gat caa ttc acg aat ttc caa gac ctc      780
Gln Ser Trp Phe Pro Ile Met Asp Gln Phe Thr Asn Phe Gln Asp Leu
        225                 230                 235

atg cca atg aag acg acg gtc caa aat tca ttg tca tac gat gat gat      828
Met Pro Met Lys Thr Thr Val Gln Asn Ser Leu Ser Tyr Asp Asp Asp
    240                 245                 250

tgt tcg aag tcc aat ttt gta tta gaa cct tat tac tcc gac ttt gct      876
Cys Ser Lys Ser Asn Phe Val Leu Glu Pro Tyr Tyr Ser Asp Phe Ala
255                 260                 265                 270

tca gtc ttg acc aca cct tct tca agc ccg act ccg tta aac tca agt      924
Ser Val Leu Thr Thr Pro Ser Ser Ser Pro Thr Pro Leu Asn Ser Ser
                275                 280                 285

tcc tca act tac atc aat agt agc act tgc agc acc gag gat gaa aaa      972
Ser Ser Thr Tyr Ile Asn Ser Ser Thr Cys Ser Thr Glu Asp Glu Lys
            290                 295                 300

gag agt tat tac agt gat aat atc act aat tat tcg ttt gat gtt aat     1020
Glu Ser Tyr Tyr Ser Asp Asn Ile Thr Asn Tyr Ser Phe Asp Val Asn
        305                 310                 315

ggt ttt ctc caa ttc caa taa acaaaacgcc attggaatag agttatgtaa        1071
Gly Phe Leu Gln Phe Gln
    320

acatgcaatc attgtatttg ttatatagat tttgttacat atccaaaatc caaaatacta   1131

tagttttaaa ataaaaaaaa aaaaaaaaaa                                    1161
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<210> 26
<211> 324
<212> PRT
<213> Arabidopsis thaliana

<400> 26

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Met Gly Arg Ser Pro Cys Cys Glu Lys Lys Asn Gly Leu Lys Lys Gly
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Pro Trp Thr Pro Glu Glu Asp Gln Lys Leu Ile Asp Tyr Ile Asn Ile
            20                  25                  30

His Gly Tyr Gly Asn Trp Arg Thr Leu Pro Lys Asn Ala Gly Leu Gln
        35                  40                  45

Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro
    50                  55                  60

Asp Ile Lys Arg Gly Arg Phe Ser Phe Glu Glu Glu Glu Thr Ile Ile
65                  70                  75                  80

Gln Leu His Ser Ile Met Gly Asn Lys Trp Ser Ala Ile Ala Ala Arg
                85                  90                  95
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Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His
100 105 110

Ile Arg Lys Arg Leu Leu Lys Met Gly Ile Asp Pro Val Thr His Thr
115 120 125

Pro Arg Leu Asp Leu Leu Asp Ile Ser Ser Ile Leu Ser Ser Ser Ile
130 135 140

Tyr Asn Ser Ser His His His His His His Gln Gln His Met Asn
145 150 155 160

Met Ser Arg Leu Met Met Ser Asp Gly Asn His Gln Pro Leu Val Asn
165 170 175

Pro Glu Ile Leu Lys Leu Ala Thr Ser Leu Phe Ser Asn Gln Asn His
180 185 190

Pro Asn Asn Thr His Glu Asn Asn Thr Val Asn Gln Thr Glu Val Asn
195 200 205

Gln Tyr Gln Thr Gly Tyr Asn Met Pro Gly Asn Glu Glu Leu Gln Ser
210 215 220

Trp Phe Pro Ile Met Asp Gln Phe Thr Asn Phe Gln Asp Leu Met Pro
225 230 235 240

Met Lys Thr Thr Val Gln Asn Ser Leu Ser Tyr Asp Asp Asp Cys Ser
245 250 255

Lys Ser Asn Phe Val Leu Glu Pro Tyr Tyr Ser Asp Phe Ala Ser Val
260 265 270

Leu Thr Thr Pro Ser Ser Ser Pro Thr Pro Leu Asn Ser Ser Ser Ser
275 280 285

Thr Tyr Ile Asn Ser Ser Thr Cys Ser Thr Glu Asp Glu Lys Glu Ser
290 295 300

Tyr Tyr Ser Asp Asn Ile Thr Asn Tyr Ser Phe Asp Val Asn Gly Phe
305 310 315 320

Leu Gln Phe Gln

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<222> (40)..(1809)
<223> G584

<400> 27
aaaaagtctt ctcttttata actacgtcag agaactgtt atg tct ccg acg aat 54
Met Ser Pro Thr Asn

MBI-17 Sequence Listing.ST25

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                                                1               5

gtt caa gta acc gat tac cat ctc aac caa tca aaa acg gat aca aca      102
Val Gln Val Thr Asp Tyr His Leu Asn Gln Ser Lys Thr Asp Thr Thr
                10                  15                  20

aat ctc tgg tca acc gac gac gat gca tcg gta atg gaa gct ttc atc      150
Asn Leu Trp Ser Thr Asp Asp Asp Ala Ser Val Met Glu Ala Phe Ile
            25                  30                  35

ggc ggc ggc tcc gat cat tct tct ctt ttt cct cca ctt cct cct cct      198
Gly Gly Gly Ser Asp His Ser Ser Leu Phe Pro Pro Leu Pro Pro Pro
        40                  45                  50

cct ctt cct caa gtc aac gaa gat aat ctc cag caa cgt ctc caa gct      246
Pro Leu Pro Gln Val Asn Glu Asp Asn Leu Gln Gln Arg Leu Gln Ala
    55                  60                  65

tta atc gaa gga gca aac gag aac tgg act tac gcc gtg ttc tgg caa      294
Leu Ile Glu Gly Ala Asn Glu Asn Trp Thr Tyr Ala Val Phe Trp Gln
70                  75                  80                  85

tca tct cac ggt ttc gcc gga gaa gac aac aac aac aac aac aca gtg      342
Ser Ser His Gly Phe Ala Gly Glu Asp Asn Asn Asn Asn Asn Thr Val
                90                  95                  100

ttg tta ggt tgg gga gat ggt tat tac aaa gga gaa gaa gag aag tct      390
Leu Leu Gly Trp Gly Asp Gly Tyr Tyr Lys Gly Glu Glu Glu Lys Ser
            105                 110                 115

aga aag aag aaa tca aat cca gct agt gca gct gaa caa gag cat cgt      438
Arg Lys Lys Lys Ser Asn Pro Ala Ser Ala Ala Glu Gln Glu His Arg
        120                 125                 130

aag aga gtg att aga gag ctc aac tct tta atc tcc ggt ggt gta gga      486
Lys Arg Val Ile Arg Glu Leu Asn Ser Leu Ile Ser Gly Gly Val Gly
    135                 140                 145

gga gga gat gaa gct gga gat gaa gaa gtt aca gat act gaa tgg ttc      534
Gly Gly Asp Glu Ala Gly Asp Glu Glu Val Thr Asp Thr Glu Trp Phe
150                 155                 160                 165

ttc tta gtt tca atg aca cag agc ttt gtc aag ggt act ggt tta cct      582
Phe Leu Val Ser Met Thr Gln Ser Phe Val Lys Gly Thr Gly Leu Pro
                170                 175                 180

ggt caa gct ttc tca aat tca gac acg att tgg tta tct ggt tct aat      630
Gly Gln Ala Phe Ser Asn Ser Asp Thr Ile Trp Leu Ser Gly Ser Asn
            185                 190                 195

gct tta gct gga tca agt tgt gag aga gct cgt caa ggt cag att tat      678
Ala Leu Ala Gly Ser Ser Cys Glu Arg Ala Arg Gln Gly Gln Ile Tyr
        200                 205                 210

ggg tta caa aca atg gtg tgt gta gcg aca gag aat ggt gtc gtt gag      726
Gly Leu Gln Thr Met Val Cys Val Ala Thr Glu Asn Gly Val Val Glu
    215                 220                 225

ctt ggt tcg tcg gag att att cat caa agt tca gat ctt gtt gat aaa      774
Leu Gly Ser Ser Glu Ile Ile His Gln Ser Ser Asp Leu Val Asp Lys
230                 235                 240                 245

gtt gac acc ttt ttc aat ttt aac aat ggt ggt ggt gaa ttt ggt tct      822
Val Asp Thr Phe Phe Asn Phe Asn Asn Gly Gly Gly Glu Phe Gly Ser
                250                 255                 260

tgg gcg ttt aat ttg aat cca gat caa gga gag aat gat cca ggt ttg      870
Trp Ala Phe Asn Leu Asn Pro Asp Gln Gly Glu Asn Asp Pro Gly Leu
            265                 270                 275

tgg att agt gaa cct aat ggt gtt gac tct ggt ctt gta gct gct ccg      918
Trp Ile Ser Glu Pro Asn Gly Val Asp Ser Gly Leu Val Ala Ala Pro
        280                 285                 290

gtg atg aat aat ggt gga aat gac tca act tct aat tct gat tct caa      966
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Val Met Asn Asn Gly Gly Asn Asp Ser Thr Ser Asn Ser Asp Ser Gln
    295                 300                 305

cca att tct aag ctt tgt aat gga agc tct gtt gaa aac cct aac cct     1014
Pro Ile Ser Lys Leu Cys Asn Gly Ser Ser Val Glu Asn Pro Asn Pro
310                 315                 320                 325

aaa gtt ctg aaa tct tgt gaa atg gtg aat ttc aag aat ggg att gag     1062
Lys Val Leu Lys Ser Cys Glu Met Val Asn Phe Lys Asn Gly Ile Glu
                330                 335                 340

aat ggt caa gaa gaa gat agt agt aat aag aag aga tca ccg gtt tcg     1110
Asn Gly Gln Glu Glu Asp Ser Ser Asn Lys Lys Arg Ser Pro Val Ser
            345                 350                 355

aat aat gaa gaa ggg atg ctt tct ttt acc tct gtt ctt cca tgt gac     1158
Asn Asn Glu Glu Gly Met Leu Ser Phe Thr Ser Val Leu Pro Cys Asp
        360                 365                 370

tcg aat cac tct gat ctt gaa gct tca gtg gct aaa gaa gct gag agt     1206
Ser Asn His Ser Asp Leu Glu Ala Ser Val Ala Lys Glu Ala Glu Ser
    375                 380                 385

aac aga gtt gtg gtt gaa ccg gag aag aaa ccg agg aaa cga ggg aga     1254
Asn Arg Val Val Val Glu Pro Glu Lys Lys Pro Arg Lys Arg Gly Arg
390                 395                 400                 405

aaa ccg gcg aat gga aga gaa gag cct ttg aat cat gta gag gca gag     1302
Lys Pro Ala Asn Gly Arg Glu Glu Pro Leu Asn His Val Glu Ala Glu
                410                 415                 420

aga cag aga aga gag aag ttg aat cag aga ttc tat tct tta aga gct     1350
Arg Gln Arg Arg Glu Lys Leu Asn Gln Arg Phe Tyr Ser Leu Arg Ala
            425                 430                 435

gtg gtt cct aat gtg tct aag atg gat aaa gct tct cta tta gga gat     1398
Val Val Pro Asn Val Ser Lys Met Asp Lys Ala Ser Leu Leu Gly Asp
        440                 445                 450

gct att tcg tat atc agt gag ctt aag tct aag ttg caa aag gct gaa     1446
Ala Ile Ser Tyr Ile Ser Glu Leu Lys Ser Lys Leu Gln Lys Ala Glu
    455                 460                 465

tct gat aaa gaa gag ttg cag aag cag att gat gtg atg aat aaa gaa     1494
Ser Asp Lys Glu Glu Leu Gln Lys Gln Ile Asp Val Met Asn Lys Glu
470                 475                 480                 485

gcg gga aat gcg aaa agt tcg gta aaa gat cga aaa tgt ttg aat caa     1542
Ala Gly Asn Ala Lys Ser Ser Val Lys Asp Arg Lys Cys Leu Asn Gln
                490                 495                 500

gaa tcg agt gtg ttg ata gag atg gag gtt gat gtg aag att att ggt     1590
Glu Ser Ser Val Leu Ile Glu Met Glu Val Asp Val Lys Ile Ile Gly
            505                 510                 515

tgg gat gca atg ata agg att caa tgt agt aag agg aat cat cct ggt     1638
Trp Asp Ala Met Ile Arg Ile Gln Cys Ser Lys Arg Asn His Pro Gly
        520                 525                 530

gct aag ttc atg gaa gca ctt aag gag ttg gat ttg gaa gtg aat cat     1686
Ala Lys Phe Met Glu Ala Leu Lys Glu Leu Asp Leu Glu Val Asn His
    535                 540                 545

gcg agt tta tcg gta gtg aat gat ctt atg atc caa caa gcg act gtg     1734
Ala Ser Leu Ser Val Val Asn Asp Leu Met Ile Gln Gln Ala Thr Val
550                 555                 560                 565

aaa atg ggg aat cag ttt ttc acg caa gat caa ctc aag gtt gct cta     1782
Lys Met Gly Asn Gln Phe Phe Thr Gln Asp Gln Leu Lys Val Ala Leu
                570                 575                 580

acg gag aaa gtt gga gaa tgt cca tga attgaagtca gcatctttag           1829
Thr Glu Lys Val Gly Glu Cys Pro
            585
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ggctaataca ccggagaata ctgcgaaaag tcgaaaacaa cgatcatagt ataagccgcg 1889

gtaaaaagtg ttaaaccttt cacacaagtt tctctagtga atgtagttgt aaactctatt 1949

gtgtaagggt aattttgtag tacccacttg ttgctattga atgcttgtta gagaggattc 2009

ttagtgtagt atatgattag gttggggttt gttgtttcat gagataaata aatgtgtttg 2069

atcaatggtt aagtctttgg tttgttggtg tatgtatgta aataaggctt ttgttagaaa 2129

taagacaaat gggactgaag ttggagttta aaa 2162

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<211> 589
<212> PRT
<213> Arabidopsis thaliana

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Met Ser Pro Thr Asn Val Gln Val Thr Asp Tyr His Leu Asn Gln Ser
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Lys Thr Asp Thr Thr Asn Leu Trp Ser Thr Asp Asp Asp Ala Ser Val
20 25 30

Met Glu Ala Phe Ile Gly Gly Gly Ser Asp His Ser Ser Leu Phe Pro
35 40 45

Pro Leu Pro Pro Pro Pro Leu Pro Gln Val Asn Glu Asp Asn Leu Gln
50 55 60

Gln Arg Leu Gln Ala Leu Ile Glu Gly Ala Asn Glu Asn Trp Thr Tyr
65 70 75 80

Ala Val Phe Trp Gln Ser Ser His Gly Phe Ala Gly Glu Asp Asn Asn
85 90 95

Asn Asn Asn Thr Val Leu Leu Gly Trp Gly Asp Gly Tyr Tyr Lys Gly
100 105 110

Glu Glu Glu Lys Ser Arg Lys Lys Lys Ser Asn Pro Ala Ser Ala Ala
115 120 125

Glu Gln Glu His Arg Lys Arg Val Ile Arg Glu Leu Asn Ser Leu Ile
130 135 140

Ser Gly Gly Val Gly Gly Gly Asp Glu Ala Gly Asp Glu Glu Val Thr
145 150 155 160

Asp Thr Glu Trp Phe Phe Leu Val Ser Met Thr Gln Ser Phe Val Lys
165 170 175

Gly Thr Gly Leu Pro Gly Gln Ala Phe Ser Asn Ser Asp Thr Ile Trp
180 185 190

Leu Ser Gly Ser Asn Ala Leu Ala Gly Ser Ser Cys Glu Arg Ala Arg
195 200 205

Gln Gly Gln Ile Tyr Gly Leu Gln Thr Met Val Cys Val Ala Thr Glu
210 215 220

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Asn Gly Val Val Glu Leu Gly Ser Ser Glu Ile Ile His Gln Ser Ser
225                 230                 235                 240

Asp Leu Val Asp Lys Val Asp Thr Phe Phe Asn Phe Asn Asn Gly Gly
                245                 250                 255

Gly Glu Phe Gly Ser Trp Ala Phe Asn Leu Asn Pro Asp Gln Gly Glu
            260                 265                 270

Asn Asp Pro Gly Leu Trp Ile Ser Glu Pro Asn Gly Val Asp Ser Gly
        275                 280                 285

Leu Val Ala Ala Pro Val Met Asn Asn Gly Gly Asn Asp Ser Thr Ser
    290                 295                 300

Asn Ser Asp Ser Gln Pro Ile Ser Lys Leu Cys Asn Gly Ser Ser Val
305                 310                 315                 320

Glu Asn Pro Asn Pro Lys Val Leu Lys Ser Cys Glu Met Val Asn Phe
                325                 330                 335

Lys Asn Gly Ile Glu Asn Gly Gln Glu Glu Asp Ser Ser Asn Lys Lys
            340                 345                 350

Arg Ser Pro Val Ser Asn Asn Glu Glu Gly Met Leu Ser Phe Thr Ser
        355                 360                 365

Val Leu Pro Cys Asp Ser Asn His Ser Asp Leu Glu Ala Ser Val Ala
    370                 375                 380

Lys Glu Ala Glu Ser Asn Arg Val Val Val Glu Pro Glu Lys Lys Pro
385                 390                 395                 400

Arg Lys Arg Gly Arg Lys Pro Ala Asn Gly Arg Glu Glu Pro Leu Asn
                405                 410                 415

His Val Glu Ala Glu Arg Gln Arg Arg Glu Lys Leu Asn Gln Arg Phe
            420                 425                 430

Tyr Ser Leu Arg Ala Val Val Pro Asn Val Ser Lys Met Asp Lys Ala
        435                 440                 445

Ser Leu Leu Gly Asp Ala Ile Ser Tyr Ile Ser Glu Leu Lys Ser Lys
    450                 455                 460

Leu Gln Lys Ala Glu Ser Asp Lys Glu Glu Leu Gln Lys Gln Ile Asp
465                 470                 475                 480

Val Met Asn Lys Glu Ala Gly Asn Ala Lys Ser Ser Val Lys Asp Arg
                485                 490                 495

Lys Cys Leu Asn Gln Glu Ser Ser Val Leu Ile Glu Met Glu Val Asp
            500                 505                 510

Val Lys Ile Ile Gly Trp Asp Ala Met Ile Arg Ile Gln Cys Ser Lys
        515                 520                 525
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Arg Asn His Pro Gly Ala Lys Phe Met Glu Ala Leu Lys Glu Leu Asp
    530                 535                 540

Leu Glu Val Asn His Ala Ser Leu Ser Val Val Asn Asp Leu Met Ile
545                 550                 555                 560

Gln Gln Ala Thr Val Lys Met Gly Asn Gln Phe Phe Thr Gln Asp Gln
                565                 570                 575

Leu Lys Val Ala Leu Thr Glu Lys Val Gly Glu Cys Pro
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<210> 29
<211> 1056
<212> DNA
<213> Arabidopsis thaliana

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<222> (1)..(1056)
<223> G668

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atg gga aga cca cct tgc tgt gaa aag att gga gtg aag aaa ggg cca       48
Met Gly Arg Pro Pro Cys Cys Glu Lys Ile Gly Val Lys Lys Gly Pro
1               5                   10                  15

tgg aca cca gag gaa gac atc atc ttg gtt tct tac atc caa gaa cat       96
Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Glu His
            20                  25                  30

ggt cct gga aac tgg aga tct gtc cca aca cac aca ggt tta aga tgt      144
Gly Pro Gly Asn Trp Arg Ser Val Pro Thr His Thr Gly Leu Arg Cys
        35                  40                  45

agc aag agc tgc aga ttg aga tgg act aat tat ctt cga ccc ggt att      192
Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly Ile
    50                  55                  60

aag cgt gga aat ttt act gag cat gaa gag aag aca att gtt cat ctt      240
Lys Arg Gly Asn Phe Thr Glu His Glu Glu Lys Thr Ile Val His Leu
65                  70                  75                  80

caa gcc ctt tta ggc aac aga tgg gca gcc ata gca tca tac ctt cca      288
Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu Pro
                85                  90                  95

gaa agg aca gac aat gat ata aag aac tat tgg aac act cac ttg aag      336
Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu Lys
            100                 105                 110

aag aag ctc aaa aag att aat gaa tct ggt gaa gaa gat aat gat ggt      384
Lys Lys Leu Lys Lys Ile Asn Glu Ser Gly Glu Glu Asp Asn Asp Gly
        115                 120                 125

gtc tct tca tca aac act agt tca caa aag aac cat caa agc act aac      432
Val Ser Ser Ser Asn Thr Ser Ser Gln Lys Asn His Gln Ser Thr Asn
    130                 135                 140

aaa ggt caa tgg gaa aga aga ctt cag aca gac att aac atg gca aaa      480
Lys Gly Gln Trp Glu Arg Arg Leu Gln Thr Asp Ile Asn Met Ala Lys
145                 150                 155                 160

caa gct ctt tgt gag gcc ttg tct tta gac aaa cca tca tcc act ctt      528
Gln Ala Leu Cys Glu Ala Leu Ser Leu Asp Lys Pro Ser Ser Thr Leu
                165                 170                 175

tca tca tct tca tca tta ccg aca cca gta atc aca caa caa aac atc      576
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Ser Ser Ser Ser Ser Leu Pro Thr Pro Val Ile Thr Gln Gln Asn Ile
            180                 185                 190

cgt aac ttc tca tca gct ttg ctt gac cgt tgt tat gat cca tcc tct      624
Arg Asn Phe Ser Ser Ala Leu Leu Asp Arg Cys Tyr Asp Pro Ser Ser
        195                 200                 205

tct tct tca tct acc aca acc acc act aca agc aac act act aat cca      672
Ser Ser Ser Ser Thr Thr Thr Thr Thr Thr Ser Asn Thr Thr Asn Pro
    210                 215                 220

tac cca tca ggg gta tat gcg tca agt gct gag aac atc gcc cgg ttg      720
Tyr Pro Ser Gly Val Tyr Ala Ser Ser Ala Glu Asn Ile Ala Arg Leu
225                 230                 235                 240

ctt caa gat ttc atg aaa gac aca ccc aag gct tta act tta tca tct      768
Leu Gln Asp Phe Met Lys Asp Thr Pro Lys Ala Leu Thr Leu Ser Ser
                245                 250                 255

tca tct ccg gtt tca gag act gga cca ctc act gct gca gtc tcg gaa      816
Ser Ser Pro Val Ser Glu Thr Gly Pro Leu Thr Ala Ala Val Ser Glu
            260                 265                 270

gaa ggt gga gaa ggg ttt gaa caa tct ttc ttc agc ttc aat tca atg      864
Glu Gly Gly Glu Gly Phe Glu Gln Ser Phe Phe Ser Phe Asn Ser Met
        275                 280                 285

gac gaa act caa aac ttg act cag gag aca agc ttc ttc cat gat caa      912
Asp Glu Thr Gln Asn Leu Thr Gln Glu Thr Ser Phe Phe His Asp Gln
    290                 295                 300

gtg atc aaa ccg gaa ata aca atg gac caa gat cat ggt cta ata tca      960
Val Ile Lys Pro Glu Ile Thr Met Asp Gln Asp His Gly Leu Ile Ser
305                 310                 315                 320

caa ggg tct ctg tct ttg ttt gag aaa tgg tta ttt gat gag caa agc     1008
Gln Gly Ser Leu Ser Leu Phe Glu Lys Trp Leu Phe Asp Glu Gln Ser
                325                 330                 335

cac gag atg gtt ggt atg gca cta gca gga caa gaa ggg atg ttc tag     1056
His Glu Met Val Gly Met Ala Leu Ala Gly Gln Glu Gly Met Phe
            340                 345                 350
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<213> Arabidopsis thaliana

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Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr Ile Gln Glu His
            20                  25                  30

Gly Pro Gly Asn Trp Arg Ser Val Pro Thr His Thr Gly Leu Arg Cys
        35                  40                  45

Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly Ile
    50                  55                  60

Lys Arg Gly Asn Phe Thr Glu His Glu Glu Lys Thr Ile Val His Leu
65                  70                  75                  80

Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu Pro
                85                  90                  95
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Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu Lys
            100                 105                 110

Lys Lys Leu Lys Lys Ile Asn Glu Ser Gly Glu Glu Asp Asn Asp Gly
        115                 120                 125

Val Ser Ser Ser Asn Thr Ser Ser Gln Lys Asn His Gln Ser Thr Asn
    130                 135                 140

Lys Gly Gln Trp Glu Arg Arg Leu Gln Thr Asp Ile Asn Met Ala Lys
145                 150                 155                 160

Gln Ala Leu Cys Glu Ala Leu Ser Leu Asp Lys Pro Ser Ser Thr Leu
                165                 170                 175

Ser Ser Ser Ser Ser Leu Pro Thr Pro Val Ile Thr Gln Gln Asn Ile
            180                 185                 190

Arg Asn Phe Ser Ser Ala Leu Leu Asp Arg Cys Tyr Asp Pro Ser Ser
        195                 200                 205

Ser Ser Ser Ser Thr Thr Thr Thr Thr Thr Ser Asn Thr Thr Asn Pro
    210                 215                 220

Tyr Pro Ser Gly Val Tyr Ala Ser Ser Ala Glu Asn Ile Ala Arg Leu
225                 230                 235                 240

Leu Gln Asp Phe Met Lys Asp Thr Pro Lys Ala Leu Thr Leu Ser Ser
                245                 250                 255

Ser Ser Pro Val Ser Glu Thr Gly Pro Leu Thr Ala Ala Val Ser Glu
            260                 265                 270

Glu Gly Gly Glu Gly Phe Glu Gln Ser Phe Phe Ser Phe Asn Ser Met
        275                 280                 285

Asp Glu Thr Gln Asn Leu Thr Gln Glu Thr Ser Phe Phe His Asp Gln
    290                 295                 300

Val Ile Lys Pro Glu Ile Thr Met Asp Gln Asp His Gly Leu Ile Ser
305                 310                 315                 320

Gln Gly Ser Leu Ser Leu Phe Glu Lys Trp Leu Phe Asp Glu Gln Ser
                325                 330                 335

His Glu Met Val Gly Met Ala Leu Ala Gly Gln Glu Gly Met Phe
            340                 345                 350


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MBI-17 Sequence Listing.ST25

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atgataagtc agattgcata cttgtctcct ccatggctac tctcaagggt tttggctgcg     180

gtggattcgt ttggtttctc tagaatctaa agaggttatc acaacggctt tgcaatttga     240

aaactttcat gtttggggag atcaaagatg gtttcttttt tatactttac ttgttagaga     300

ggatttgaag cagcgaatag ctgcaaccgg tcctgtt atg gat act aat aca tct      355
                                          Met Asp Thr Asn Thr Ser
                                          1               5

gga gaa gaa tta tta gct aag gca aga aag cca tat aca ata aca aag       403
Gly Glu Glu Leu Leu Ala Lys Ala Arg Lys Pro Tyr Thr Ile Thr Lys
            10                  15                  20

cag cga gag cga tgg act gag gat gag cat gag agg ttt cta gaa gcc       451
Gln Arg Glu Arg Trp Thr Glu Asp Glu His Glu Arg Phe Leu Glu Ala
        25                  30                  35

ttg agg ctt tat gga aga gct tgg caa cga att gaa gaa cat att ggg       499
Leu Arg Leu Tyr Gly Arg Ala Trp Gln Arg Ile Glu Glu His Ile Gly
    40                  45                  50

aca aag act gct gtt cag atc aga agt cat gca caa aag ttc ttc aca       547
Thr Lys Thr Ala Val Gln Ile Arg Ser His Ala Gln Lys Phe Phe Thr
55                  60                  65                  70

aag ttg gag aaa gag gct gaa gtt aaa ggc atc cct gtt tgc caa gct       595
Lys Leu Glu Lys Glu Ala Glu Val Lys Gly Ile Pro Val Cys Gln Ala
                75                  80                  85

ttg gac ata gaa att ccg cct cct cgt cct aaa cga aaa ccc aat act       643
Leu Asp Ile Glu Ile Pro Pro Pro Arg Pro Lys Arg Lys Pro Asn Thr
            90                  95                  100

cct tat cct cga aaa cct ggg aac aac ggt aca tct tcc tct caa gta       691
Pro Tyr Pro Arg Lys Pro Gly Asn Asn Gly Thr Ser Ser Ser Gln Val
        105                 110                 115

tca tca gca aaa gat gca aaa ctt gtt tca tcg gcc tct tct tca cag       739
Ser Ser Ala Lys Asp Ala Lys Leu Val Ser Ser Ala Ser Ser Ser Gln
    120                 125                 130

ttg aat cag gcg ttc ttg gat ttg gaa aaa atg ccg ttc tct gag aaa       787
Leu Asn Gln Ala Phe Leu Asp Leu Glu Lys Met Pro Phe Ser Glu Lys
135                 140                 145                 150

aca tca act gga aaa gaa aat caa gat gag aat tgc tcg ggt gtt tct       835
Thr Ser Thr Gly Lys Glu Asn Gln Asp Glu Asn Cys Ser Gly Val Ser
                155                 160                 165

act gtg aac aag tat ccc tta cca acg aaa cag gta agt ggc gac att       883
Thr Val Asn Lys Tyr Pro Leu Pro Thr Lys Gln Val Ser Gly Asp Ile
            170                 175                 180

gaa aca agt aag acc tca act gtg gac aac gcg gtt caa gat gtt ccc       931
Glu Thr Ser Lys Thr Ser Thr Val Asp Asn Ala Val Gln Asp Val Pro
        185                 190                 195

aag aag aac aaa gac aaa gat ggt aac gat ggt act act gtg cac agc       979
Lys Lys Asn Lys Asp Lys Asp Gly Asn Asp Gly Thr Thr Val His Ser
    200                 205                 210

atg caa aac tac cct tgg cat ttc cac gca gat att gtg aac ggg aat      1027
Met Gln Asn Tyr Pro Trp His Phe His Ala Asp Ile Val Asn Gly Asn
215                 220                 225                 230

ata gca aaa tgc cct caa aat cat ccc tca ggt atg gta tct caa gac      1075
Ile Ala Lys Cys Pro Gln Asn His Pro Ser Gly Met Val Ser Gln Asp
                235                 240                 245
```

```
ttc atg ttt cat cct atg aga gaa gaa act cac ggg cac gca aat ctt     1123
Phe Met Phe His Pro Met Arg Glu Glu Thr His Gly His Ala Asn Leu
            250                 255                 260

caa gct aca aca gca tct gct act act aca gct tct cat caa gcg ttt     1171
Gln Ala Thr Thr Ala Ser Ala Thr Thr Thr Ala Ser His Gln Ala Phe
        265                 270                 275

cca gct tgt cat tca cag gat gat tac cgt tcg ttt ctc cag ata tca     1219
Pro Ala Cys His Ser Gln Asp Asp Tyr Arg Ser Phe Leu Gln Ile Ser
    280                 285                 290

tct act ttc tcc aat ctt att atg tca act ctc cta cag aat cct gca     1267
Ser Thr Phe Ser Asn Leu Ile Met Ser Thr Leu Leu Gln Asn Pro Ala
295                 300                 305                 310

gct cat gct gca gct aca ttc gct gct tcg gtc tgg cct tat gcg agt     1315
Ala His Ala Ala Ala Thr Phe Ala Ala Ser Val Trp Pro Tyr Ala Ser
                315                 320                 325

gtc ggg aat tct ggt gat tca tca acc cca atg agc tct tct cct cca     1363
Val Gly Asn Ser Gly Asp Ser Ser Thr Pro Met Ser Ser Ser Pro Pro
            330                 335                 340

agt ata act gcc att gcc gct gct aca gta gct gct gca act gct tgg     1411
Ser Ile Thr Ala Ile Ala Ala Ala Thr Val Ala Ala Ala Thr Ala Trp
        345                 350                 355

tgg gct tct cat gga ctt ctt cct gta tgc gct cca gct cca ata aca     1459
Trp Ala Ser His Gly Leu Leu Pro Val Cys Ala Pro Ala Pro Ile Thr
    360                 365                 370

tgt gtt cca ttc tca act gtt gca gtt cca act cca gca atg act gaa     1507
Cys Val Pro Phe Ser Thr Val Ala Val Pro Thr Pro Ala Met Thr Glu
375                 380                 385                 390

atg gat acc gtt gaa aat act caa ccg ttt gag aaa caa aac aca gct     1555
Met Asp Thr Val Glu Asn Thr Gln Pro Phe Glu Lys Gln Asn Thr Ala
                395                 400                 405

ctg caa gat caa acc ttg gct tcg aaa tct cca gct tca tca tct gat     1603
Leu Gln Asp Gln Thr Leu Ala Ser Lys Ser Pro Ala Ser Ser Ser Asp
            410                 415                 420

gat tca gat gag act gga gta acc aag cta aat gcc gac tca aaa acc     1651
Asp Ser Asp Glu Thr Gly Val Thr Lys Leu Asn Ala Asp Ser Lys Thr
        425                 430                 435

aat gat gat aaa att gag gag gtt gtt gtt act gcc gct gtg cat gac     1699
Asn Asp Asp Lys Ile Glu Glu Val Val Val Thr Ala Ala Val His Asp
    440                 445                 450

tca aac act gcc cag aag aaa aat ctt gtg gac cgc tca tcg tgt ggc     1747
Ser Asn Thr Ala Gln Lys Lys Asn Leu Val Asp Arg Ser Ser Cys Gly
455                 460                 465                 470

tca aat aca cct tca ggg agt gac gca gaa act gat gca tta gat aaa     1795
Ser Asn Thr Pro Ser Gly Ser Asp Ala Glu Thr Asp Ala Leu Asp Lys
                475                 480                 485

atg gag aaa gat aaa gag gat gtg aag gag aca gat gag aat cag cca     1843
Met Glu Lys Asp Lys Glu Asp Val Lys Glu Thr Asp Glu Asn Gln Pro
            490                 495                 500

gat gtt att gag tta aat aac cgt aag att aaa atg aga gac aac aac     1891
Asp Val Ile Glu Leu Asn Asn Arg Lys Ile Lys Met Arg Asp Asn Asn
        505                 510                 515

agc aac aac aat gca act act gat tcg tgg aag gaa gtc tcc gaa gag     1939
Ser Asn Asn Asn Ala Thr Thr Asp Ser Trp Lys Glu Val Ser Glu Glu
    520                 525                 530

ggt cgt ata gcg ttt cag gct ctc ttt gca aga gaa aga ttg cct caa     1987
Gly Arg Ile Ala Phe Gln Ala Leu Phe Ala Arg Glu Arg Leu Pro Gln
535                 540                 545                 550
```

```
agc ttt tcg cct cct caa gtg gca gag aat gtg aat aga aaa caa agt     2035
Ser Phe Ser Pro Pro Gln Val Ala Glu Asn Val Asn Arg Lys Gln Ser
                555                 560                 565

gac acg tca atg cca ttg gct cct aat ttc aaa agc cag gat tct tgt     2083
Asp Thr Ser Met Pro Leu Ala Pro Asn Phe Lys Ser Gln Asp Ser Cys
            570                 575                 580

gct gca gac caa gaa gga gta gta atg atc ggt gtt gga aca tgc aag     2131
Ala Ala Asp Gln Glu Gly Val Val Met Ile Gly Val Gly Thr Cys Lys
        585                 590                 595

agt ctt aaa acg aga cag aca gga ttt aag cca tac aag aga tgt tca     2179
Ser Leu Lys Thr Arg Gln Thr Gly Phe Lys Pro Tyr Lys Arg Cys Ser
    600                 605                 610

atg gaa gtg aaa gag agc caa gtt ggg aac ata aac aat caa agt gat     2227
Met Glu Val Lys Glu Ser Gln Val Gly Asn Ile Asn Asn Gln Ser Asp
615                 620                 625                 630

gaa aaa gtc tgc aaa agg ctt cga ttg gaa gga gaa gct tct aca tga     2275
Glu Lys Val Cys Lys Arg Leu Arg Leu Glu Gly Glu Ala Ser Thr
                635                 640                 645

cagacttgga ggtaaaaaaa aaacatccac atttttatca atatctttaa atctagtgtt   2335

agtagtttgc ttctccaatc tttatgaaag agacttttaa ttttccttcc gaacatttct   2395

ttggtcatgt caggttctgt accatattac cccatgtctt gtctcttgtc tctgtttgtg   2455

tatgctactt gtggtctata tgtcatctgc tactactgtt aattaaccat taagcaatgg   2515

atttgtcttt a                                                       2526
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<210> 32
<211> 645
<212> PRT
<213> Arabidopsis thaliana

<400> 32

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Met Asp Thr Asn Thr Ser Gly Glu Glu Leu Leu Ala Lys Ala Arg Lys
1               5                   10                  15

Pro Tyr Thr Ile Thr Lys Gln Arg Glu Arg Trp Thr Glu Asp Glu His
            20                  25                  30

Glu Arg Phe Leu Glu Ala Leu Arg Leu Tyr Gly Arg Ala Trp Gln Arg
        35                  40                  45

Ile Glu Glu His Ile Gly Thr Lys Thr Ala Val Gln Ile Arg Ser His
    50                  55                  60

Ala Gln Lys Phe Phe Thr Lys Leu Glu Lys Glu Ala Glu Val Lys Gly
65                  70                  75                  80

Ile Pro Val Cys Gln Ala Leu Asp Ile Glu Ile Pro Pro Pro Arg Pro
                85                  90                  95

Lys Arg Lys Pro Asn Thr Pro Tyr Pro Arg Lys Pro Gly Asn Asn Gly
            100                 105                 110

Thr Ser Ser Ser Gln Val Ser Ser Ala Lys Asp Ala Lys Leu Val Ser
        115                 120                 125
```

```
Ser Ala Ser Ser Ser Gln Leu Asn Gln Ala Phe Leu Asp Leu Glu Lys
    130                 135                 140

Met Pro Phe Ser Glu Lys Thr Ser Thr Gly Lys Glu Asn Gln Asp Glu
145                 150                 155                 160

Asn Cys Ser Gly Val Ser Thr Val Asn Lys Tyr Pro Leu Pro Thr Lys
                165                 170                 175

Gln Val Ser Gly Asp Ile Glu Thr Ser Lys Thr Ser Thr Val Asp Asn
            180                 185                 190

Ala Val Gln Asp Val Pro Lys Lys Asn Lys Asp Lys Asp Gly Asn Asp
        195                 200                 205

Gly Thr Thr Val His Ser Met Gln Asn Tyr Pro Trp His Phe His Ala
    210                 215                 220

Asp Ile Val Asn Gly Asn Ile Ala Lys Cys Pro Gln Asn His Pro Ser
225                 230                 235                 240

Gly Met Val Ser Gln Asp Phe Met Phe His Pro Met Arg Glu Glu Thr
                245                 250                 255

His Gly His Ala Asn Leu Gln Ala Thr Thr Ala Ser Ala Thr Thr Thr
            260                 265                 270

Ala Ser His Gln Ala Phe Pro Ala Cys His Ser Gln Asp Asp Tyr Arg
        275                 280                 285

Ser Phe Leu Gln Ile Ser Ser Thr Phe Ser Asn Leu Ile Met Ser Thr
    290                 295                 300

Leu Leu Gln Asn Pro Ala Ala His Ala Ala Ala Thr Phe Ala Ala Ser
305                 310                 315                 320

Val Trp Pro Tyr Ala Ser Val Gly Asn Ser Gly Asp Ser Ser Thr Pro
                325                 330                 335

Met Ser Ser Ser Pro Pro Ser Ile Thr Ala Ile Ala Ala Ala Thr Val
            340                 345                 350

Ala Ala Ala Thr Ala Trp Trp Ala Ser His Gly Leu Leu Pro Val Cys
        355                 360                 365

Ala Pro Ala Pro Ile Thr Cys Val Pro Phe Ser Thr Val Ala Val Pro
    370                 375                 380

Thr Pro Ala Met Thr Glu Met Asp Thr Val Glu Asn Thr Gln Pro Phe
385                 390                 395                 400

Glu Lys Gln Asn Thr Ala Leu Gln Asp Gln Thr Leu Ala Ser Lys Ser
                405                 410                 415

Pro Ala Ser Ser Ser Asp Asp Ser Asp Glu Thr Gly Val Thr Lys Leu
            420                 425                 430
```

```
Asn Ala Asp Ser Lys Thr Asn Asp Asp Lys Ile Glu Glu Val Val Val
        435                 440                 445

Thr Ala Ala Val His Asp Ser Asn Thr Ala Gln Lys Lys Asn Leu Val
    450                 455                 460

Asp Arg Ser Ser Cys Gly Ser Asn Thr Pro Ser Gly Ser Asp Ala Glu
465                 470                 475                 480

Thr Asp Ala Leu Asp Lys Met Glu Lys Asp Lys Glu Asp Val Lys Glu
                485                 490                 495

Thr Asp Glu Asn Gln Pro Asp Val Ile Glu Leu Asn Asn Arg Lys Ile
            500                 505                 510

Lys Met Arg Asp Asn Asn Ser Asn Asn Asn Ala Thr Thr Asp Ser Trp
        515                 520                 525

Lys Glu Val Ser Glu Glu Gly Arg Ile Ala Phe Gln Ala Leu Phe Ala
    530                 535                 540

Arg Glu Arg Leu Pro Gln Ser Phe Ser Pro Pro Gln Val Ala Glu Asn
545                 550                 555                 560

Val Asn Arg Lys Gln Ser Asp Thr Ser Met Pro Leu Ala Pro Asn Phe
                565                 570                 575

Lys Ser Gln Asp Ser Cys Ala Ala Asp Gln Glu Gly Val Val Met Ile
            580                 585                 590

Gly Val Gly Thr Cys Lys Ser Leu Lys Thr Arg Gln Thr Gly Phe Lys
        595                 600                 605

Pro Tyr Lys Arg Cys Ser Met Glu Val Lys Glu Ser Gln Val Gly Asn
    610                 615                 620

Ile Asn Asn Gln Ser Asp Glu Lys Val Cys Lys Arg Leu Arg Leu Glu
625                 630                 635                 640

Gly Glu Ala Ser Thr
                645
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<210> 33
<211> 228
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(228)
<223> G682

<400> 33

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atg gat aac cat cgc agg act aag caa ccc aag acc aac tcc atc gtt       48
Met Asp Asn His Arg Arg Thr Lys Gln Pro Lys Thr Asn Ser Ile Val
1               5                   10                  15

act tct tct tct gaa gaa gtg agt agt ctt gag tgg gaa gtt gtg aac       96
Thr Ser Ser Ser Glu Glu Val Ser Ser Leu Glu Trp Glu Val Val Asn
```

20 25 30

atg agt caa gaa gaa gaa gat ttg gtc tct cga atg cat aag ctt gtc 144
Met Ser Gln Glu Glu Glu Asp Leu Val Ser Arg Met His Lys Leu Val
35 40 45

ggt gac agg tgg gaa ctg ata gct ggg agg atc cca gga aga acc gct 192
Gly Asp Arg Trp Glu Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr Ala
50 55 60

gga gaa att gag agg ttt tgg gtc atg aaa aat tga 228
Gly Glu Ile Glu Arg Phe Trp Val Met Lys Asn
65 70 75

<210> 34
<211> 75
<212> PRT
<213> Arabidopsis thaliana

<400> 34

Met Asp Asn His Arg Arg Thr Lys Gln Pro Lys Thr Asn Ser Ile Val
1 5 10 15

Thr Ser Ser Ser Glu Glu Val Ser Ser Leu Glu Trp Glu Val Val Asn
20 25 30

Met Ser Gln Glu Glu Glu Asp Leu Val Ser Arg Met His Lys Leu Val
35 40 45

Gly Asp Arg Trp Glu Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr Ala
50 55 60

Gly Glu Ile Glu Arg Phe Trp Val Met Lys Asn
65 70 75

<210> 35
<211> 584
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (157)..(441)
<223> G225

<400> 35
ctctctctct cactcttttc ttttccgaga acccaacaaa aaaaaagcta ctattaatcc 60

ttcccctcgt gaggaaatca tttcttcttg tttctcgaga tttattctct ttctctctct 120

ctttctctgt gtgtttcgtg tcttcagatt agttcg atg ttt cgt tca gac aag 174
Met Phe Arg Ser Asp Lys
1 5

gcg gaa aaa atg gat aaa cga cga cgg aga cag agc aaa gcc aag gct 222
Ala Glu Lys Met Asp Lys Arg Arg Arg Arg Gln Ser Lys Ala Lys Ala
10 15 20

tct tgt tcc gaa gag gtg agt agt atc gaa tgg gaa gct gtg aag atg 270
Ser Cys Ser Glu Glu Val Ser Ser Ile Glu Trp Glu Ala Val Lys Met
25 30 35

tca gaa gaa gaa gaa gat ctc att tct cgg atg tat aaa ctc gtt ggc 318
Ser Glu Glu Glu Glu Asp Leu Ile Ser Arg Met Tyr Lys Leu Val Gly
40 45 50

gac agg tgg gag ttg atc gcc gga agg atc ccg gga cgg acg ccg gag 366

```
Asp Arg Trp Glu Leu Ile Ala Gly Arg Ile Pro Gly Arg Thr Pro Glu
55                  60                  65                  70

gag ata gag aga tat tgg ctt atg aaa cac ggc gtc gtt ttt gcc aac      414
Glu Ile Glu Arg Tyr Trp Leu Met Lys His Gly Val Val Phe Ala Asn
                75                  80                  85

aga cga aga gac ttt ttt agg aaa tga ttttttttgt ttggattaaa           461
Arg Arg Arg Asp Phe Phe Arg Lys
            90

agaaaatttt cctctcctta attcacaaga caagaaaaaa aggaaatgta cctgtccttg   521

aattactatt ttggaatgta taattatcta tatatataag aagaaaaaat tgcttaggaa   581

ttt                                                                 584
```

<210> 36
<211> 94
<212> PRT
<213> Arabidopsis thaliana

<400> 36

```
Met Phe Arg Ser Asp Lys Ala Glu Lys Met Asp Lys Arg Arg Arg Arg
1               5                   10                  15

Gln Ser Lys Ala Lys Ala Ser Cys Ser Glu Glu Val Ser Ser Ile Glu
            20                  25                  30

Trp Glu Ala Val Lys Met Ser Glu Glu Glu Glu Asp Leu Ile Ser Arg
        35                  40                  45

Met Tyr Lys Leu Val Gly Asp Arg Trp Glu Leu Ile Ala Gly Arg Ile
    50                  55                  60

Pro Gly Arg Thr Pro Glu Glu Ile Glu Arg Tyr Trp Leu Met Lys His
65                  70                  75                  80

Gly Val Val Phe Ala Asn Arg Arg Arg Asp Phe Phe Arg Lys
                85                  90
```

<210> 37
<211> 1369
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (104)..(1174)
<223> G678

<400> 37

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ggttgtgtcg tcactttact tctctttaaa taatctcttt ctctagtgat tgactttagg     60

aacaagtgaa gtgagtgatt tttaataatc gccggccgag aga atg gga agg gcg      115
                                                Met Gly Arg Ala
                                                1

ccg tgc tgt gag aag gta gga att aag aag ggg cgc tgg acg gcg gag      163
Pro Cys Cys Glu Lys Val Gly Ile Lys Lys Gly Arg Trp Thr Ala Glu
5                   10                  15                  20

gaa gac cgg act ctc tcc gac tac att cag tcc aac ggc gaa gga tca      211
Glu Asp Arg Thr Leu Ser Asp Tyr Ile Gln Ser Asn Gly Glu Gly Ser
                25                  30                  35
```

```
tgg cgt tct ctt ccc aaa aat gcc ggg cta aag aga tgt gga aag agc      259
Trp Arg Ser Leu Pro Lys Asn Ala Gly Leu Lys Arg Cys Gly Lys Ser
            40                  45                  50

tgt aga ttg aga tgg ata aac tat ttg aga tca gac atc aag aga gga      307
Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Ser Asp Ile Lys Arg Gly
        55                  60                  65

aac ata act ccc gaa gaa gag gac gtc att gtt aaa ctg cat tcc act      355
Asn Ile Thr Pro Glu Glu Glu Asp Val Ile Val Lys Leu His Ser Thr
    70                  75                  80

ttg gga acc agg tgg tca aca att gcg agc aat cta ccg gga aga aca      403
Leu Gly Thr Arg Trp Ser Thr Ile Ala Ser Asn Leu Pro Gly Arg Thr
85                  90                  95                  100

gac aac gaa ata aaa aac tat tgg aat tct cat ctc agc cgt aaa ctc      451
Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu Ser Arg Lys Leu
                105                 110                 115

cac ggt tac ttc aga aaa cca act gtc gcc aat acc gtc gag aat gcg      499
His Gly Tyr Phe Arg Lys Pro Thr Val Ala Asn Thr Val Glu Asn Ala
            120                 125                 130

cct ccg cct cct aag cgt aga cct gga aga acc agc aga tcc gcc atg      547
Pro Pro Pro Pro Lys Arg Arg Pro Gly Arg Thr Ser Arg Ser Ala Met
        135                 140                 145

aaa ccc aaa ttt atc cta aac cct aaa aac cac aaa acc cct aat tct      595
Lys Pro Lys Phe Ile Leu Asn Pro Lys Asn His Lys Thr Pro Asn Ser
    150                 155                 160

ttt aaa gca aac aaa agt gac atc gtt ttg cca act acg aca ata gag      643
Phe Lys Ala Asn Lys Ser Asp Ile Val Leu Pro Thr Thr Thr Ile Glu
165                 170                 175                 180

aat gga gag gga gac aaa gaa gac gca tta atg gtg ttg tca agt agt      691
Asn Gly Glu Gly Asp Lys Glu Asp Ala Leu Met Val Leu Ser Ser Ser
                185                 190                 195

agc tta agt gga gca gag gaa ccc ggt tta gga cca tgt ggt tat gga      739
Ser Leu Ser Gly Ala Glu Glu Pro Gly Leu Gly Pro Cys Gly Tyr Gly
            200                 205                 210

gac gat ggc gat tgt aac cca agc att aat ggc gac gat gga gct ttg      787
Asp Asp Gly Asp Cys Asn Pro Ser Ile Asn Gly Asp Asp Gly Ala Leu
        215                 220                 225

tgt ctc aat gac gac att ttc gat tct tgt ttt cta ttg gac gac tct      835
Cys Leu Asn Asp Asp Ile Phe Asp Ser Cys Phe Leu Leu Asp Asp Ser
    230                 235                 240

cat gct gtc cac gtg tcc tca tgt gag tcg aac aac gta aaa aac tct      883
His Ala Val His Val Ser Ser Cys Glu Ser Asn Asn Val Lys Asn Ser
245                 250                 255                 260

gag cca tat gga ggg atg tca gtt ggg cac aaa aat atc gaa acg atg      931
Glu Pro Tyr Gly Gly Met Ser Val Gly His Lys Asn Ile Glu Thr Met
                265                 270                 275

gct gat gat ttc gtt gac tgg gac ttt gta tgg aga gaa ggt caa acc      979
Ala Asp Asp Phe Val Asp Trp Asp Phe Val Trp Arg Glu Gly Gln Thr
            280                 285                 290

ctt tgg gac gaa aaa gag gat ctt gat tcg gtt ttg tcg agg ctg tta     1027
Leu Trp Asp Glu Lys Glu Asp Leu Asp Ser Val Leu Ser Arg Leu Leu
        295                 300                 305

gat gga gag gaa atg gaa tct gag atc aga caa agg gac tcc aac gac     1075
Asp Gly Glu Glu Met Glu Ser Glu Ile Arg Gln Arg Asp Ser Asn Asp
    310                 315                 320

ttt gga gaa ccg ttg gat att gac gaa gaa aac aag atg gct gct tgg     1123
Phe Gly Glu Pro Leu Asp Ile Asp Glu Glu Asn Lys Met Ala Ala Trp
325                 330                 335                 340
```

ctt ttt tcc tta aaa att tta ccc cct tcc ttt tcc ctt ttc ccc ctt 1171
Leu Phe Ser Leu Lys Ile Leu Pro Pro Ser Phe Ser Leu Phe Pro Leu
345 350 355

taa tttttaccaa aacccccccc tgccagatcc tgtccgtttt tccattaaac 1224

ctttttctcc ccctaccttc ctttttttat ttttaatttt tttttttcc ttttttttc 1284

ctttcctttt ttaattccga tttttggcgg gttgccaatt aaccaaatta aatccatcct 1344

taaaaaaaaa aaaaaaaaaa aaaaa 1369

<210> 38
<211> 356
<212> PRT
<213> Arabidopsis thaliana

<400> 38

Met Gly Arg Ala Pro Cys Cys Glu Lys Val Gly Ile Lys Lys Gly Arg
1 5 10 15

Trp Thr Ala Glu Glu Asp Arg Thr Leu Ser Asp Tyr Ile Gln Ser Asn
20 25 30

Gly Glu Gly Ser Trp Arg Ser Leu Pro Lys Asn Ala Gly Leu Lys Arg
35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Ser Asp
50 55 60

Ile Lys Arg Gly Asn Ile Thr Pro Glu Glu Glu Asp Val Ile Val Lys
65 70 75 80

Leu His Ser Thr Leu Gly Thr Arg Trp Ser Thr Ile Ala Ser Asn Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Ser His Leu
100 105 110

Ser Arg Lys Leu His Gly Tyr Phe Arg Lys Pro Thr Val Ala Asn Thr
115 120 125

Val Glu Asn Ala Pro Pro Pro Pro Lys Arg Arg Pro Gly Arg Thr Ser
130 135 140

Arg Ser Ala Met Lys Pro Lys Phe Ile Leu Asn Pro Lys Asn His Lys
145 150 155 160

Thr Pro Asn Ser Phe Lys Ala Asn Lys Ser Asp Ile Val Leu Pro Thr
165 170 175

Thr Thr Ile Glu Asn Gly Glu Gly Asp Lys Glu Asp Ala Leu Met Val
180 185 190

Leu Ser Ser Ser Ser Leu Ser Gly Ala Glu Glu Pro Gly Leu Gly Pro
195 200 205

Cys Gly Tyr Gly Asp Asp Gly Asp Cys Asn Pro Ser Ile Asn Gly Asp
210 215 220

```
Asp Gly Ala Leu Cys Leu Asn Asp Asp Ile Phe Asp Ser Cys Phe Leu
225                 230                 235                 240

Leu Asp Asp Ser His Ala Val His Val Ser Ser Cys Glu Ser Asn Asn
                245                 250                 255

Val Lys Asn Ser Glu Pro Tyr Gly Gly Met Ser Val Gly His Lys Asn
            260                 265                 270

Ile Glu Thr Met Ala Asp Asp Phe Val Asp Trp Asp Phe Val Trp Arg
        275                 280                 285

Glu Gly Gln Thr Leu Trp Asp Glu Lys Glu Asp Leu Asp Ser Val Leu
    290                 295                 300

Ser Arg Leu Leu Asp Gly Glu Glu Met Glu Ser Glu Ile Arg Gln Arg
305                 310                 315                 320

Asp Ser Asn Asp Phe Gly Glu Pro Leu Asp Ile Asp Glu Glu Asn Lys
                325                 330                 335

Met Ala Ala Trp Leu Phe Ser Leu Lys Ile Leu Pro Pro Ser Phe Ser
            340                 345                 350

Leu Phe Pro Leu
        355
```

<210> 39
<211> 1046
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (46)..(867)
<223> G233

<400> 39

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gaaaaacatt tcaacttctt ttatcagcaa tcacaaatca aagag atg gga aga gct     57
                                                 Met Gly Arg Ala
                                                 1

cca tgc tgt gag aag atg ggg ttg aag aga gga cca tgg aca cct gaa      105
Pro Cys Cys Glu Lys Met Gly Leu Lys Arg Gly Pro Trp Thr Pro Glu
5                   10                  15                  20

gaa gat caa atc ttg gtc tct ttt atc ctc aac cat gga cat agt aac      153
Glu Asp Gln Ile Leu Val Ser Phe Ile Leu Asn His Gly His Ser Asn
                25                  30                  35

tgg cga gcc ctc cct aag caa gct ggt ctt ttg aga tgt gga aaa agc      201
Trp Arg Ala Leu Pro Lys Gln Ala Gly Leu Leu Arg Cys Gly Lys Ser
            40                  45                  50

tgt aga ctt agg tgg atg aac tat tta aag cct gat att aaa cgt ggc      249
Cys Arg Leu Arg Trp Met Asn Tyr Leu Lys Pro Asp Ile Lys Arg Gly
        55                  60                  65

aat ttc acc aaa gaa gag gaa gat gct atc atc agc tta cac caa ata      297
Asn Phe Thr Lys Glu Glu Glu Asp Ala Ile Ile Ser Leu His Gln Ile
    70                  75                  80

ctt ggc aat aga tgg tca gcg att gca gca aaa ctg cct gga aga acc      345
```

```
Leu Gly Asn Arg Trp Ser Ala Ile Ala Ala Lys Leu Pro Gly Arg Thr
85                  90                  95                  100

gat aac gag atc aag aac gta tgg cac act cac ttg aag aag aga ctc      393
Asp Asn Glu Ile Lys Asn Val Trp His Thr His Leu Lys Lys Arg Leu
                105                 110                 115

gaa gat tat caa cca gct aaa cct aag acc agc aac aaa aag aag ggt      441
Glu Asp Tyr Gln Pro Ala Lys Pro Lys Thr Ser Asn Lys Lys Lys Gly
            120                 125                 130

act aaa cca aaa tct gaa tcc gta ata acg agc tcg aac agt act aga      489
Thr Lys Pro Lys Ser Glu Ser Val Ile Thr Ser Ser Asn Ser Thr Arg
        135                 140                 145

agc gaa tcg gag cta gca gat tca tca aac cct tct gga gaa agc tta      537
Ser Glu Ser Glu Leu Ala Asp Ser Ser Asn Pro Ser Gly Glu Ser Leu
    150                 155                 160

ttt tcg aca tcg cct tcg aca agt gag gtt tct tcg atg aca ctc ata      585
Phe Ser Thr Ser Pro Ser Thr Ser Glu Val Ser Ser Met Thr Leu Ile
165                 170                 175                 180

agc cac gac ggc tat agc aac gag att aat atg gat aac aaa ccg gga      633
Ser His Asp Gly Tyr Ser Asn Glu Ile Asn Met Asp Asn Lys Pro Gly
                185                 190                 195

gat atc agt act atc gat caa gaa tgt gtt tct ttc gaa act ttt ggt      681
Asp Ile Ser Thr Ile Asp Gln Glu Cys Val Ser Phe Glu Thr Phe Gly
            200                 205                 210

gcg gat atc gat gaa agc ttc tgg aaa gag aca ctg tat agc caa gat      729
Ala Asp Ile Asp Glu Ser Phe Trp Lys Glu Thr Leu Tyr Ser Gln Asp
        215                 220                 225

gaa cac aac tac gta tcg aat gac cta gaa gtc gct ggt tta gtt gag      777
Glu His Asn Tyr Val Ser Asn Asp Leu Glu Val Ala Gly Leu Val Glu
    230                 235                 240

ata caa caa gag ttt caa aac ttg ggc tcc gct aat aat gag atg att      825
Ile Gln Gln Glu Phe Gln Asn Leu Gly Ser Ala Asn Asn Glu Met Ile
245                 250                 255                 260

ttt gac agt gag atg gaa ctt ctg gtt cga tgt att ggc tag              867
Phe Asp Ser Glu Met Glu Leu Leu Val Arg Cys Ile Gly
                265                 270

aaccggcggg gaacaagatc tcttagccgg gctctagtta acatgtttga ggagtaaagt    927

gaaatggtgc aaattagtta aggctaagaa attcaaaagc ttttgtttac cgagaaaaaa    987

acacactcta actcttgatg tgatgtagtt agtgtattaa ttagaggctg cgttttcaa    1046


<210>  40
<211>  273
<212>  PRT
<213>  Arabidopsis thaliana

<400>  40

Met Gly Arg Ala Pro Cys Cys Glu Lys Met Gly Leu Lys Arg Gly Pro
1               5                   10                  15


Trp Thr Pro Glu Glu Asp Gln Ile Leu Val Ser Phe Ile Leu Asn His
            20                  25                  30


Gly His Ser Asn Trp Arg Ala Leu Pro Lys Gln Ala Gly Leu Leu Arg
        35                  40                  45


Cys Gly Lys Ser Cys Arg Leu Arg Trp Met Asn Tyr Leu Lys Pro Asp
    50                  55                  60
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Ile Lys Arg Gly Asn Phe Thr Lys Glu Glu Glu Asp Ala Ile Ile Ser
65 70 75 80

Leu His Gln Ile Leu Gly Asn Arg Trp Ser Ala Ile Ala Ala Lys Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Val Trp His Thr His Leu
100 105 110

Lys Lys Arg Leu Glu Asp Tyr Gln Pro Ala Lys Pro Lys Thr Ser Asn
115 120 125

Lys Lys Lys Gly Thr Lys Pro Lys Ser Glu Ser Val Ile Thr Ser Ser
130 135 140

Asn Ser Thr Arg Ser Glu Ser Glu Leu Ala Asp Ser Ser Asn Pro Ser
145 150 155 160

Gly Glu Ser Leu Phe Ser Thr Ser Pro Ser Thr Ser Glu Val Ser Ser
165 170 175

Met Thr Leu Ile Ser His Asp Gly Tyr Ser Asn Glu Ile Asn Met Asp
180 185 190

Asn Lys Pro Gly Asp Ile Ser Thr Ile Asp Gln Glu Cys Val Ser Phe
195 200 205

Glu Thr Phe Gly Ala Asp Ile Asp Glu Ser Phe Trp Lys Glu Thr Leu
210 215 220

Tyr Ser Gln Asp Glu His Asn Tyr Val Ser Asn Asp Leu Glu Val Ala
225 230 235 240

Gly Leu Val Glu Ile Gln Gln Glu Phe Gln Asn Leu Gly Ser Ala Asn
245 250 255

Asn Glu Met Ile Phe Asp Ser Glu Met Glu Leu Leu Val Arg Cys Ile
260 265 270

Gly

<210> 41
<211> 1262
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (217)..(957)
<223> G463

<400> 41
ctcgagctac gtcaggggtc tctttctgtt tgtttgtttt cttgtttcct tctctctctc 60

tctttctttc tttgtcttcc tttcccaggt tgtttttttt tgctctctct gccttcttga 120

ctttcaaaag actctttctt tcttttggat tgattttgga ttctagggct ctctttcttt 180

MBI-17 Sequence Listing.ST25

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tagtgggttt ttgttgttgt tgttgtggtc tctctg atg att act gaa ctt gag      234
                                        Met Ile Thr Glu Leu Glu
                                        1               5

atg ggg aaa ggt gag agt gag ctt gag ctt ggt cta ggg ctg agt ctt      282
Met Gly Lys Gly Glu Ser Glu Leu Glu Leu Gly Leu Gly Leu Ser Leu
            10                  15                  20

ggc ggt gga acg gcg gcc aag att ggt aaa tca ggt ggt ggt ggc gcg      330
Gly Gly Gly Thr Ala Ala Lys Ile Gly Lys Ser Gly Gly Gly Gly Ala
        25                  30                  35

tgg gga gag cgt gga agg ctt ttg acg gct aag gat ttt cct tct gtt      378
Trp Gly Glu Arg Gly Arg Leu Leu Thr Ala Lys Asp Phe Pro Ser Val
    40                  45                  50

ggt tct aaa cgt gct gct gat tct gct tct cat gct ggt tca tct cct      426
Gly Ser Lys Arg Ala Ala Asp Ser Ala Ser His Ala Gly Ser Ser Pro
55                  60                  65                  70

cct cgt tca agt caa gtt gtt gga tgg cct cct ata ggg tca cac agg      474
Pro Arg Ser Ser Gln Val Val Gly Trp Pro Pro Ile Gly Ser His Arg
                75                  80                  85

atg aac agt ttg gtt aat aac caa gct aca aag tca gca aga gaa gaa      522
Met Asn Ser Leu Val Asn Asn Gln Ala Thr Lys Ser Ala Arg Glu Glu
            90                  95                  100

gaa gaa gct ggt aag aag aaa gtg aaa gat gat gaa cct aaa gat gtg      570
Glu Glu Ala Gly Lys Lys Lys Val Lys Asp Asp Glu Pro Lys Asp Val
        105                 110                 115

aca aag aaa gtg aat ggg aaa gta caa gtt gga ttt att aag gtg aac      618
Thr Lys Lys Val Asn Gly Lys Val Gln Val Gly Phe Ile Lys Val Asn
    120                 125                 130

atg gat gga gtt gct ata gga aga aaa gtg gat ttg aat gct cat tct      666
Met Asp Gly Val Ala Ile Gly Arg Lys Val Asp Leu Asn Ala His Ser
135                 140                 145                 150

tct tac gag aat ttg gcg caa aca ttg gaa gat atg ttc ttt cgc act      714
Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu Asp Met Phe Phe Arg Thr
                155                 160                 165

aat ccg ggt act gtc ggg tta acc agt cag ttc act aaa ccg ttg agg      762
Asn Pro Gly Thr Val Gly Leu Thr Ser Gln Phe Thr Lys Pro Leu Arg
            170                 175                 180

ctt tta gat gga tcg tct gag ttt gta ctt act tat gaa gat aag gaa      810
Leu Leu Asp Gly Ser Ser Glu Phe Val Leu Thr Tyr Glu Asp Lys Glu
        185                 190                 195

gga gat tgg atg ctt gtt ggt gat gtt cca tgg aga atg ttc atc aac      858
Gly Asp Trp Met Leu Val Gly Asp Val Pro Trp Arg Met Phe Ile Asn
    200                 205                 210

tcg gtg aaa agg cta cgt gtg atg aaa acc tct gaa gct aat gga ctc      906
Ser Val Lys Arg Leu Arg Val Met Lys Thr Ser Glu Ala Asn Gly Leu
215                 220                 225                 230

gct gca cga aat caa gaa cca aac gag aga cag cga aag cag ccg gtt      954
Ala Ala Arg Asn Gln Glu Pro Asn Glu Arg Gln Arg Lys Gln Pro Val
                235                 240                 245

tag atctcttttc gacgttacgg tgttacaggt tttatatttt ggggttttgc          1007

aagtctgaga tacttctgaa gcaagcataa gctagattga tcttatatcc agtttgtgta   1067

ttttcttggt tcttataatg gtttttactg gttttcttta gttttttttt ttgctgtctt   1127

ttaattttcg gttgcgattt cactatatac tatggatgga agagaatgct ctttatatct   1187

tttactacac tgtaaatatt tgaagcttat ctaatatcgt ttttaagggt taaaaaaccc   1247
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tgacgtagcc tcgag 1262

<210> 42
<211> 246
<212> PRT
<213> Arabidopsis thaliana

<400> 42

Met Ile Thr Glu Leu Glu Met Gly Lys Gly Glu Ser Glu Leu Glu Leu
1 5 10 15

Gly Leu Gly Leu Ser Leu Gly Gly Gly Thr Ala Ala Lys Ile Gly Lys
20 25 30

Ser Gly Gly Gly Gly Ala Trp Gly Glu Arg Gly Arg Leu Leu Thr Ala
35 40 45

Lys Asp Phe Pro Ser Val Gly Ser Lys Arg Ala Ala Asp Ser Ala Ser
50 55 60

His Ala Gly Ser Ser Pro Pro Arg Ser Ser Gln Val Val Gly Trp Pro
65 70 75 80

Pro Ile Gly Ser His Arg Met Asn Ser Leu Val Asn Asn Gln Ala Thr
85 90 95

Lys Ser Ala Arg Glu Glu Glu Glu Ala Gly Lys Lys Lys Val Lys Asp
100 105 110

Asp Glu Pro Lys Asp Val Thr Lys Lys Val Asn Gly Lys Val Gln Val
115 120 125

Gly Phe Ile Lys Val Asn Met Asp Gly Val Ala Ile Gly Arg Lys Val
130 135 140

Asp Leu Asn Ala His Ser Ser Tyr Glu Asn Leu Ala Gln Thr Leu Glu
145 150 155 160

Asp Met Phe Phe Arg Thr Asn Pro Gly Thr Val Gly Leu Thr Ser Gln
165 170 175

Phe Thr Lys Pro Leu Arg Leu Leu Asp Gly Ser Ser Glu Phe Val Leu
180 185 190

Thr Tyr Glu Asp Lys Glu Gly Asp Trp Met Leu Val Gly Asp Val Pro
195 200 205

Trp Arg Met Phe Ile Asn Ser Val Lys Arg Leu Arg Val Met Lys Thr
210 215 220

Ser Glu Ala Asn Gly Leu Ala Ala Arg Asn Gln Glu Pro Asn Glu Arg
225 230 235 240

Gln Arg Lys Gln Pro Val
245

<210> 43

MBI-17 Sequence Listing.ST25

<211> 741
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(741)
<223> G2422

<400> 43

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atg ggc gaa tca ccc aaa ggg ttg aga aaa ggt aca tgg act act gaa        48
Met Gly Glu Ser Pro Lys Gly Leu Arg Lys Gly Thr Trp Thr Thr Glu
1               5                  10                  15

gaa gat att ctc ttg agg caa tgc att gat aag tat gga gaa ggc aaa        96
Glu Asp Ile Leu Leu Arg Gln Cys Ile Asp Lys Tyr Gly Glu Gly Lys
            20                  25                  30

tgg cat cga gtt cct tta aga act ggt ctc aat cgg tgc cga aag agt       144
Trp His Arg Val Pro Leu Arg Thr Gly Leu Asn Arg Cys Arg Lys Ser
        35                  40                  45

tgt aga ctt aga tgg ttg aat tat ttg aag cca agt att aag aga gga       192
Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
    50                  55                  60

aaa ctc tgc tcc gat gaa gtt gat ctt gtt ctt cgc ctt cat aaa ctt       240
Lys Leu Cys Ser Asp Glu Val Asp Leu Val Leu Arg Leu His Lys Leu
65                  70                  75                  80

cta gga aat agg tgg tcc ttg atc gct ggt aga ttg cct ggt cgg act       288
Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
                85                  90                  95

gct aat gat gtc aag aat tac tgg aac act cat ttg agt aag aag cac       336
Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
            100                 105                 110

gat gaa cga tgc tgt aag acg aag atg ata aac aaa aac att act tct       384
Asp Glu Arg Cys Cys Lys Thr Lys Met Ile Asn Lys Asn Ile Thr Ser
        115                 120                 125

cat cct act tca tcg gcc caa aaa atc gat gtt tta aag cct cgg cct       432
His Pro Thr Ser Ser Ala Gln Lys Ile Asp Val Leu Lys Pro Arg Pro
    130                 135                 140

cga tcc ttc tcc gat aaa aat agt tgc aac gat gtc aat atc ttg cca       480
Arg Ser Phe Ser Asp Lys Asn Ser Cys Asn Asp Val Asn Ile Leu Pro
145                 150                 155                 160

aaa gtt gac gtt gtt cct tta cat ctt gga ctc aac aac aat tat gtt       528
Lys Val Asp Val Val Pro Leu His Leu Gly Leu Asn Asn Asn Tyr Val
                165                 170                 175

tgt gaa agt agt att aca tgt aac aaa gat gag caa aaa gat aag ctt       576
Cys Glu Ser Ser Ile Thr Cys Asn Lys Asp Glu Gln Lys Asp Lys Leu
            180                 185                 190

att aat att aat cta ttg gat gga gat aat atg tgg tgg gaa agt tta       624
Ile Asn Ile Asn Leu Leu Asp Gly Asp Asn Met Trp Trp Glu Ser Leu
        195                 200                 205

ctg gag gca gat gtg ttg ggt cca gaa gct acg gaa aca gca aag ggt       672
Leu Glu Ala Asp Val Leu Gly Pro Glu Ala Thr Glu Thr Ala Lys Gly
    210                 215                 220

gtg acc tta ccg ctt gac ttt gag caa att tgg gct cgg ttt gat gaa       720
Val Thr Leu Pro Leu Asp Phe Glu Gln Ile Trp Ala Arg Phe Asp Glu
225                 230                 235                 240

gag act tta gaa ctg aat tag                                          741
Glu Thr Leu Glu Leu Asn
                245
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<210> 44
<211> 246
<212> PRT
<213> Arabidopsis thaliana

<400> 44

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Met Gly Glu Ser Pro Lys Gly Leu Arg Lys Gly Thr Trp Thr Thr Glu
1               5                  10                  15

Glu Asp Ile Leu Leu Arg Gln Cys Ile Asp Lys Tyr Gly Glu Gly Lys
            20                  25                  30

Trp His Arg Val Pro Leu Arg Thr Gly Leu Asn Arg Cys Arg Lys Ser
        35                  40                  45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
    50                  55                  60

Lys Leu Cys Ser Asp Glu Val Asp Leu Val Leu Arg Leu His Lys Leu
65                  70                  75                  80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
                85                  90                  95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
            100                 105                 110

Asp Glu Arg Cys Cys Lys Thr Lys Met Ile Asn Lys Asn Ile Thr Ser
        115                 120                 125

His Pro Thr Ser Ser Ala Gln Lys Ile Asp Val Leu Lys Pro Arg Pro
    130                 135                 140

Arg Ser Phe Ser Asp Lys Asn Ser Cys Asn Asp Val Asn Ile Leu Pro
145                 150                 155                 160

Lys Val Asp Val Val Pro Leu His Leu Gly Leu Asn Asn Asn Tyr Val
                165                 170                 175

Cys Glu Ser Ser Ile Thr Cys Asn Lys Asp Glu Gln Lys Asp Lys Leu
            180                 185                 190

Ile Asn Ile Asn Leu Leu Asp Gly Asp Asn Met Trp Trp Glu Ser Leu
        195                 200                 205

Leu Glu Ala Asp Val Leu Gly Pro Glu Ala Thr Glu Thr Ala Lys Gly
    210                 215                 220

Val Thr Leu Pro Leu Asp Phe Glu Gln Ile Trp Ala Arg Phe Asp Glu
225                 230                 235                 240

Glu Thr Leu Glu Leu Asn
                245
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<210> 45
<211> 762
<212> DNA

<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(630)
<223> G2421

<400> 45

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atg gag ggt tcg tcc aaa ggg ttg agg aaa ggt gca tgg act gct gaa       48
Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu
1               5                  10                  15

gaa gat agt ctc ttg agg cag tgt att ggt aag tat gga gaa ggc aaa       96
Glu Asp Ser Leu Leu Arg Gln Cys Ile Gly Lys Tyr Gly Glu Gly Lys
            20                  25                  30

tgg cat caa gtt cct tta aga gct ggg cta aat cgg tgc agg aaa agt      144
Trp His Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
        35                  40                  45

tgt aga cta aga tgg tta aac tat ttg aag cca agt atc aag aga gga      192
Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
    50                  55                  60

aaa ttt agt tct gat gaa gtt gat ctt ctt ctt cgt ctt cat aag ctt      240
Lys Phe Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu
65                  70                  75                  80

cta gga aat agg tgg tcc ttg att gct ggt cga tta cct ggt cgg acc      288
Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
                85                  90                  95

gct aat gat gtc aag aac tac tgg aac acc cat ctg agt aag aag cat      336
Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
            100                 105                 110

gaa ccg tgt tgt aaa act aag ata aaa agg ata aat att ata acc cct      384
Glu Pro Cys Cys Lys Thr Lys Ile Lys Arg Ile Asn Ile Ile Thr Pro
        115                 120                 125

cct aat aca ccg gcc caa aaa gtt tgt gaa aat agt atc aca tgt aac      432
Pro Asn Thr Pro Ala Gln Lys Val Cys Glu Asn Ser Ile Thr Cys Asn
    130                 135                 140

aaa gat gat gag aaa gat gat ttt gtg gat aat ttt atg gtt gga gat      480
Lys Asp Asp Glu Lys Asp Asp Phe Val Asp Asn Phe Met Val Gly Asp
145                 150                 155                 160

aat ata tgg ttg gag cgt ttg cta gac gag ggc caa gag gta gat gtg      528
Asn Ile Trp Leu Glu Arg Leu Leu Asp Glu Gly Gln Glu Val Asp Val
                165                 170                 175

ctg gtt aca gaa gcg gcg gca aca gaa aag gag ggc act ttg gcg ttt      576
Leu Val Thr Glu Ala Ala Ala Thr Glu Lys Glu Gly Thr Leu Ala Phe
            180                 185                 190

gac gtt gag caa ctt tgg aat ttg ttc gat gga gag act gtg atc ttt      624
Asp Val Glu Gln Leu Trp Asn Leu Phe Asp Gly Glu Thr Val Ile Phe
        195                 200                 205

gat tag tgtttataaa cgtttgtgtt ctcttgtttg tgaggtttct ctatttaatt       680
Asp

tagtatctat tttctaaatt aactaatatc ttatagtatt ttaggcaaac cttatgtttc    740

cgtttctgtg cggccgctct ag                                            762
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<210> 46
<211> 209
<212> PRT
<213> Arabidopsis thaliana

<400> 46

Met Glu Gly Ser Ser Lys Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu
1 5 10 15

Glu Asp Ser Leu Leu Arg Gln Cys Ile Gly Lys Tyr Gly Glu Gly Lys
20 25 30

Trp His Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
35 40 45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
50 55 60

Lys Phe Ser Ser Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu
65 70 75 80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
85 90 95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
100 105 110

Glu Pro Cys Cys Lys Thr Lys Ile Lys Arg Ile Asn Ile Ile Thr Pro
115 120 125

Pro Asn Thr Pro Ala Gln Lys Val Cys Glu Asn Ser Ile Thr Cys Asn
130 135 140

Lys Asp Asp Glu Lys Asp Asp Phe Val Asp Asn Phe Met Val Gly Asp
145 150 155 160

Asn Ile Trp Leu Glu Arg Leu Leu Asp Glu Gly Gln Glu Val Asp Val
165 170 175

Leu Val Thr Glu Ala Ala Ala Thr Glu Lys Glu Gly Thr Leu Ala Phe
180 185 190

Asp Val Glu Gln Leu Trp Asn Leu Phe Asp Gly Glu Thr Val Ile Phe
195 200 205

Asp

<210> 47
<211> 1665
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (33)..(1376)
<223> G772

<400> 47
aaaaaccaaa accggttttt ttttttcttt tt atg ggt cgc gaa tct ctg gct 53
Met Gly Arg Glu Ser Leu Ala
1 5

gtt gtg tcc tcg ccg cca tcg gcg act gcg ccc agt act gct gtg tcg 101

```
Val Val Ser Ser Pro Pro Ser Ala Thr Ala Pro Ser Thr Ala Val Ser
        10                  15                  20

gct acc tcg ctt gct cct ggc ttt cga ttt cat ccg act gat gag gaa      149
Ala Thr Ser Leu Ala Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu
    25                  30                  35

ctc gtg agc tat tac ttg aag agg aag gtt ctg ggt aaa cct gta cgc      197
Leu Val Ser Tyr Tyr Leu Lys Arg Lys Val Leu Gly Lys Pro Val Arg
40                  45                  50                  55

ttc gat gcg att gga gag gta gat atc tac aag cat gag ccc tgg gat      245
Phe Asp Ala Ile Gly Glu Val Asp Ile Tyr Lys His Glu Pro Trp Asp
                60                  65                  70

tta gca gtg ttt tcg aag ttg aaa act cgg gac caa gaa tgg tac ttc      293
Leu Ala Val Phe Ser Lys Leu Lys Thr Arg Asp Gln Glu Trp Tyr Phe
            75                  80                  85

ttc agt gcg tta gat aag aag tac ggt aat ggt gct agg atg aat cga      341
Phe Ser Ala Leu Asp Lys Lys Tyr Gly Asn Gly Ala Arg Met Asn Arg
        90                  95                  100

gca act aac aaa ggg tac tgg aaa gca act gga aaa gac aga gaa atc      389
Ala Thr Asn Lys Gly Tyr Trp Lys Ala Thr Gly Lys Asp Arg Glu Ile
    105                 110                 115

cgc cgg gat att cag ttg ctc ggt atg aaa aag acg ctt gtt ttc cac      437
Arg Arg Asp Ile Gln Leu Leu Gly Met Lys Lys Thr Leu Val Phe His
120                 125                 130                 135

agc ggg cgt gct cca gac ggc ctt cgg act aat tgg gtc atg cac gag      485
Ser Gly Arg Ala Pro Asp Gly Leu Arg Thr Asn Trp Val Met His Glu
                140                 145                 150

tat cgc ctt gtg gaa tat gaa act gaa act aac gga agc ctg ctg cag      533
Tyr Arg Leu Val Glu Tyr Glu Thr Glu Thr Asn Gly Ser Leu Leu Gln
            155                 160                 165

gat gca tat gtg ttg tgc aga gtg ttt cac aag aat aac att ggg cca      581
Asp Ala Tyr Val Leu Cys Arg Val Phe His Lys Asn Asn Ile Gly Pro
        170                 175                 180

cca agt ggg aac aga tat gcg cca ttc atg gaa gaa gaa tgg gct gat      629
Pro Ser Gly Asn Arg Tyr Ala Pro Phe Met Glu Glu Glu Trp Ala Asp
    185                 190                 195

ggt gga gga gct ctg att cca gga ata gac gtt agg gtc agg gta gag      677
Gly Gly Gly Ala Leu Ile Pro Gly Ile Asp Val Arg Val Arg Val Glu
200                 205                 210                 215

gct cta cca caa gcc aat gga aac aac cag atg gac cag gaa atg cat      725
Ala Leu Pro Gln Ala Asn Gly Asn Asn Gln Met Asp Gln Glu Met His
                220                 225                 230

tca gca agc aag gat ctc att aac atc aac gag cta ccg aga gat gct      773
Ser Ala Ser Lys Asp Leu Ile Asn Ile Asn Glu Leu Pro Arg Asp Ala
            235                 240                 245

act cca atg gac atc gaa cct aac caa cag aat cat cat gag agt gcc      821
Thr Pro Met Asp Ile Glu Pro Asn Gln Gln Asn His His Glu Ser Ala
        250                 255                 260

ttc aag cca cag gag agt aac aac cat agt ggt tat gaa gaa gat gag      869
Phe Lys Pro Gln Glu Ser Asn Asn His Ser Gly Tyr Glu Glu Asp Glu
    265                 270                 275

gac aca ctc aaa cgc gag cac gca gaa gaa gat gag cgt cct cct tct      917
Asp Thr Leu Lys Arg Glu His Ala Glu Glu Asp Glu Arg Pro Pro Ser
280                 285                 290                 295

cta tgc att ctc aac aaa gaa gct cca cta cct ctc ctg caa tac aaa      965
Leu Cys Ile Leu Asn Lys Glu Ala Pro Leu Pro Leu Leu Gln Tyr Lys
                300                 305                 310
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cgt aga cgc caa aac gag tcc aac aac aac tca agc agg aac aca cag     1013
Arg Arg Arg Gln Asn Glu Ser Asn Asn Asn Ser Ser Arg Asn Thr Gln
            315                 320                 325

gac cat tgt tcg tcc aca ata aca acc gtc gac aat aca acc acc tta     1061
Asp His Cys Ser Ser Thr Ile Thr Thr Val Asp Asn Thr Thr Thr Leu
        330                 335                 340

atc tca tca tct gct gct gct gct acc aac act gcc atc tct gca ttg     1109
Ile Ser Ser Ser Ala Ala Ala Ala Thr Asn Thr Ala Ile Ser Ala Leu
    345                 350                 355

ctt gag ttc tca ctt atg ggt atc tcc gac aag aaa gaa aac cag cag     1157
Leu Glu Phe Ser Leu Met Gly Ile Ser Asp Lys Lys Glu Asn Gln Gln
360                 365                 370                 375

aaa gag gaa act tct cct cct agt cca att gca tct cct gaa gag aag     1205
Lys Glu Glu Thr Ser Pro Pro Ser Pro Ile Ala Ser Pro Glu Glu Lys
                380                 385                 390

gtt aat gat ctc cag aag gag gtt cac cag atg tct gtt gaa aga gaa     1253
Val Asn Asp Leu Gln Lys Glu Val His Gln Met Ser Val Glu Arg Glu
            395                 400                 405

act ttc aag ctt gag atg atg agt gca gag gct atg atc agc att ctc     1301
Thr Phe Lys Leu Glu Met Met Ser Ala Glu Ala Met Ile Ser Ile Leu
        410                 415                 420

cag tca aga atc gat gcg ctg cgt cag gag aac gag gaa ctt aag aag     1349
Gln Ser Arg Ile Asp Ala Leu Arg Gln Glu Asn Glu Glu Leu Lys Lys
    425                 430                 435

aag aac gcc agt gga caa gct agt taa accaccgcaa catctctcca           1396
Lys Asn Ala Ser Gly Gln Ala Ser
440                 445

ggtgtcttct tcttcttctt cttcttcttt gcctcttagc tgtaatcttc ttaatagtat   1456

gagctatgga tgtagcttct tcagacggat cagaaacctt atgaatctct gttgtaaaat   1516

taggataaaa cggaacggag ccaaccaact aggtcttttt attttatcct tttttacttt   1576

ggatgtttct gcatcttttg ggaacatttt caggctgatc cattgtcgta tattatcatc   1636

tatctatcta gtcttttcag acaaaaaaa                                     1665
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<210> 48
<211> 447
<212> PRT
<213> Arabidopsis thaliana

<400> 48

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Met Gly Arg Glu Ser Leu Ala Val Val Ser Ser Pro Pro Ser Ala Thr
1               5                   10                  15

Ala Pro Ser Thr Ala Val Ser Ala Thr Ser Leu Ala Pro Gly Phe Arg
            20                  25                  30

Phe His Pro Thr Asp Glu Glu Leu Val Ser Tyr Tyr Leu Lys Arg Lys
        35                  40                  45

Val Leu Gly Lys Pro Val Arg Phe Asp Ala Ile Gly Glu Val Asp Ile
    50                  55                  60

Tyr Lys His Glu Pro Trp Asp Leu Ala Val Phe Ser Lys Leu Lys Thr
65                  70                  75                  80

Arg Asp Gln Glu Trp Tyr Phe Phe Ser Ala Leu Asp Lys Lys Tyr Gly
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85 90 95

Asn Gly Ala Arg Met Asn Arg Ala Thr Asn Lys Gly Tyr Trp Lys Ala
100 105 110

Thr Gly Lys Asp Arg Glu Ile Arg Arg Asp Ile Gln Leu Leu Gly Met
115 120 125

Lys Lys Thr Leu Val Phe His Ser Gly Arg Ala Pro Asp Gly Leu Arg
130 135 140

Thr Asn Trp Val Met His Glu Tyr Arg Leu Val Glu Tyr Glu Thr Glu
145 150 155 160

Thr Asn Gly Ser Leu Leu Gln Asp Ala Tyr Val Leu Cys Arg Val Phe
165 170 175

His Lys Asn Asn Ile Gly Pro Pro Ser Gly Asn Arg Tyr Ala Pro Phe
180 185 190

Met Glu Glu Glu Trp Ala Asp Gly Gly Gly Ala Leu Ile Pro Gly Ile
195 200 205

Asp Val Arg Val Arg Val Glu Ala Leu Pro Gln Ala Asn Gly Asn Asn
210 215 220

Gln Met Asp Gln Glu Met His Ser Ala Ser Lys Asp Leu Ile Asn Ile
225 230 235 240

Asn Glu Leu Pro Arg Asp Ala Thr Pro Met Asp Ile Glu Pro Asn Gln
245 250 255

Gln Asn His His Glu Ser Ala Phe Lys Pro Gln Glu Ser Asn Asn His
260 265 270

Ser Gly Tyr Glu Glu Asp Glu Asp Thr Leu Lys Arg Glu His Ala Glu
275 280 285

Glu Asp Glu Arg Pro Pro Ser Leu Cys Ile Leu Asn Lys Glu Ala Pro
290 295 300

Leu Pro Leu Leu Gln Tyr Lys Arg Arg Arg Gln Asn Glu Ser Asn Asn
305 310 315 320

Asn Ser Ser Arg Asn Thr Gln Asp His Cys Ser Ser Thr Ile Thr Thr
325 330 335

Val Asp Asn Thr Thr Thr Leu Ile Ser Ser Ser Ala Ala Ala Ala Thr
340 345 350

Asn Thr Ala Ile Ser Ala Leu Leu Glu Phe Ser Leu Met Gly Ile Ser
355 360 365

Asp Lys Lys Glu Asn Gln Gln Lys Glu Glu Thr Ser Pro Pro Ser Pro
370 375 380

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Ile Ala Ser Pro Glu Glu Lys Val Asn Asp Leu Gln Lys Glu Val His
385                 390                 395                 400

Gln Met Ser Val Glu Arg Glu Thr Phe Lys Leu Glu Met Met Ser Ala
                405                 410                 415

Glu Ala Met Ile Ser Ile Leu Gln Ser Arg Ile Asp Ala Leu Arg Gln
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Thr Val Asp Ile Met Arg Leu Pro Lys Met Glu Asp Gln Thr Ala Ile
            5                   10                  15

caa gaa gct gca tca caa ggc tta aaa agc atg gaa cac ttg att cgt      154
Gln Glu Ala Ala Ser Gln Gly Leu Lys Ser Met Glu His Leu Ile Arg
        20                  25                  30

gtc ctc tct aac cgt ccc gaa gaa cgt aac gtt gat tgc tct gag atc      202
Val Leu Ser Asn Arg Pro Glu Glu Arg Asn Val Asp Cys Ser Glu Ile
    35                  40                  45

act gat ttc aca gtt tct aag ttc aag aaa gtt atc tct ctt ctt aac      250
Thr Asp Phe Thr Val Ser Lys Phe Lys Lys Val Ile Ser Leu Leu Asn
50                  55                  60                  65

cgt tcc ggt cac gcc cgg ttt aga cgt ggt ccg gtt cat tcc cct cct      298
Arg Ser Gly His Ala Arg Phe Arg Arg Gly Pro Val His Ser Pro Pro
                70                  75                  80

tcc tcc tcc gtt cct cca ccg gtg aaa gtg aca act ccg gct ccc act      346
Ser Ser Ser Val Pro Pro Pro Val Lys Val Thr Thr Pro Ala Pro Thr
            85                  90                  95

cag atc tct gct cca gca ccg gtt agc ttc gtt cag gca aat caa caa      394
Gln Ile Ser Ala Pro Ala Pro Val Ser Phe Val Gln Ala Asn Gln Gln
        100                 105                 110

agc gtg acg tta gat ttc act aga ccg agc gtt ttt ggc gct aaa acc      442
Ser Val Thr Leu Asp Phe Thr Arg Pro Ser Val Phe Gly Ala Lys Thr
    115                 120                 125

aag agc tcg gag gtt gtt gag ttt gct aaa gag agc ttt agc gta tct      490
Lys Ser Ser Glu Val Val Glu Phe Ala Lys Glu Ser Phe Ser Val Ser
130                 135                 140                 145

tct aac tct tct ttc atg tct tct gcg atc acc ggt gat gga agt gtc      538
Ser Asn Ser Ser Phe Met Ser Ser Ala Ile Thr Gly Asp Gly Ser Val
                150                 155                 160

tct aaa ggc tct tcg atc ttt ctt gct ccg gct cca gcg gtg cca gtg      586
Ser Lys Gly Ser Ser Ile Phe Leu Ala Pro Ala Pro Ala Val Pro Val
            165                 170                 175
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Thr Ser Ser Gly Lys Pro Pro Leu Ser Gly Leu Pro Tyr Arg Lys Arg
180 185 190

tgc ttt gaa cat gac cac tct gaa ggc ttt tcc ggc aag atc tct ggc 682
Cys Phe Glu His Asp His Ser Glu Gly Phe Ser Gly Lys Ile Ser Gly
195 200 205

tcc ggc aac ggc aag tgc cat tgc aag aaa agc cga aaa aat cgg atg 730
Ser Gly Asn Gly Lys Cys His Cys Lys Lys Ser Arg Lys Asn Arg Met
210 215 220 225

aag aga acc gtg aga gta ccg gcg gta agt gca aag atc gcc gat ata 778
Lys Arg Thr Val Arg Val Pro Ala Val Ser Ala Lys Ile Ala Asp Ile
230 235 240

cca cca gac gaa tat tca tgg aga aag tat gga caa aaa ccg atc aaa 826
Pro Pro Asp Glu Tyr Ser Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys
245 250 255

ggc tca cca cat cca cgg ggt tat tac aag tgt agt aca ttt aga gga 874
Gly Ser Pro His Pro Arg Gly Tyr Tyr Lys Cys Ser Thr Phe Arg Gly
260 265 270

tgt cca gcg agg aaa cac gtg gaa aga gct ttg gat gat tca acg atg 922
Cys Pro Ala Arg Lys His Val Glu Arg Ala Leu Asp Asp Ser Thr Met
275 280 285

ttg att gtg acg tac gaa gga gag cac cgt cat cac cag tcc acg atg 970
Leu Ile Val Thr Tyr Glu Gly Glu His Arg His His Gln Ser Thr Met
290 295 300 305

cag gag cat gta act cct agc gtg agt ggt ttg gtg ttt ggt tcg gct 1018
Gln Glu His Val Thr Pro Ser Val Ser Gly Leu Val Phe Gly Ser Ala
310 315 320

tga agaattaatt agtttggtag ttttgtaata ttttgagaaa tagaggggtt 1071

ggttttgtaa ttttttttct ataacaaaat tagttttaga ttttttttta gtagtctttt 1131

gaatggattt taatcttact accgagaaag aaaaaattct tactacattt tcaaaaaaaa 1191

aaaaaaa 1198

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35 40 45

Ile Thr Asp Phe Thr Val Ser Lys Phe Lys Lys Val Ile Ser Leu Leu
50 55 60

Asn Arg Ser Gly His Ala Arg Phe Arg Arg Gly Pro Val His Ser Pro
65 70 75 80

Pro Ser Ser Ser Val Pro Pro Pro Val Lys Val Thr Thr Pro Ala Pro
85 90 95

Thr Gln Ile Ser Ala Pro Ala Pro Val Ser Phe Val Gln Ala Asn Gln
100 105 110

Gln Ser Val Thr Leu Asp Phe Thr Arg Pro Ser Val Phe Gly Ala Lys
115 120 125

Thr Lys Ser Ser Glu Val Val Glu Phe Ala Lys Glu Ser Phe Ser Val
130 135 140

Ser Ser Asn Ser Ser Phe Met Ser Ser Ala Ile Thr Gly Asp Gly Ser
145 150 155 160

Val Ser Lys Gly Ser Ser Ile Phe Leu Ala Pro Ala Pro Ala Val Pro
165 170 175

Val Thr Ser Ser Gly Lys Pro Pro Leu Ser Gly Leu Pro Tyr Arg Lys
180 185 190

Arg Cys Phe Glu His Asp His Ser Glu Gly Phe Ser Gly Lys Ile Ser
195 200 205

Gly Ser Gly Asn Gly Lys Cys His Cys Lys Lys Ser Arg Lys Asn Arg
210 215 220

Met Lys Arg Thr Val Arg Val Pro Ala Val Ser Ala Lys Ile Ala Asp
225 230 235 240

Ile Pro Pro Asp Glu Tyr Ser Trp Arg Lys Tyr Gly Gln Lys Pro Ile
245 250 255

Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr Lys Cys Ser Thr Phe Arg
260 265 270

Gly Cys Pro Ala Arg Lys His Val Glu Arg Ala Leu Asp Asp Ser Thr
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Met Leu Ile Val Thr Tyr Glu Gly Glu His Arg His His Gln Ser Thr
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ttttttcttca tcatttttat tctccttctt cttctgctgt tcatttctcc aggttaca 178

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atg atg ttt aat gag atg gga atg tgt gga aac atg gat ttc ttc tct   226
Met Met Phe Asn Glu Met Gly Met Cys Gly Asn Met Asp Phe Phe Ser
1               5                  10                  15

tct gga tca ctt ggt gaa gtt gat ttc tgt cct gtt cca caa gct gag   274
Ser Gly Ser Leu Gly Glu Val Asp Phe Cys Pro Val Pro Gln Ala Glu
            20                  25                  30

cct gat tcc att gtt gaa gat gac tat act gat gat gag att gat gtt   322
Pro Asp Ser Ile Val Glu Asp Asp Tyr Thr Asp Asp Glu Ile Asp Val
        35                  40                  45

gat gaa ttg gag agg agg atg tgg aga gac aaa atg cgg ctt aaa cgt   370
Asp Glu Leu Glu Arg Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
    50                  55                  60

ctc aag gag cag gat aag ggt aaa gaa ggt gtt gat gct gct aaa cag   418
Leu Lys Glu Gln Asp Lys Gly Lys Glu Gly Val Asp Ala Ala Lys Gln
65                  70                  75                  80

agg cag tct caa gag caa gct agg agg aag aaa atg tct aga gct caa   466
Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala Gln
                85                  90                  95

gat ggg atc ttg aag tat atg ttg aag atg atg gaa gtt tgt aaa gct   514
Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys Ala
            100                 105                 110

caa ggc ttt gtt tat ggg att att ccg gag aat ggg aag cct gtg act   562
Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Asn Gly Lys Pro Val Thr
        115                 120                 125

ggt gct tct gat aat tta agg gag tgg tgg aaa gat aag gtt agg ttt   610
Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg Phe
    130                 135                 140

gat cgt aat ggt cct gcg gct att acc aag tat caa gcg gag aat aat   658
Asp Arg Asn Gly Pro Ala Ala Ile Thr Lys Tyr Gln Ala Glu Asn Asn
145                 150                 155                 160

atc ccg ggg att cat gaa ggt aat aac ccg att gga ccg act cct cat   706
Ile Pro Gly Ile His Glu Gly Asn Asn Pro Ile Gly Pro Thr Pro His
                165                 170                 175

acc ttg caa gag ctt caa gac acg act ctt gga tcg ctt ttg tct gcg   754
Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu Ser Ala
            180                 185                 190

ttg atg caa cac tgt gat cct cct cag aga cgt ttt cct ttg gag aaa   802
Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu Glu Lys
        195                 200                 205

gga gtt cct cct ccg tgg tgg cct aat ggg aaa gag gat tgg tgg cct   850
Gly Val Pro Pro Pro Trp Trp Pro Asn Gly Lys Glu Asp Trp Trp Pro
    210                 215                 220

caa ctt ggt ttg cct aaa gat caa ggt cct gca cct tac aag aag cct   898
Gln Leu Gly Leu Pro Lys Asp Gln Gly Pro Ala Pro Tyr Lys Lys Pro
225                 230                 235                 240

cat gat ttg aag aag gcg tgg aaa gtc ggc gtt ttg act gcg gtt atc   946
His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala Val Ile
                245                 250                 255

aag cat atg ttt cct gat att gct aag atc cgt aag ctc gtg agg caa   994
Lys His Met Phe Pro Asp Ile Ala Lys Ile Arg Lys Leu Val Arg Gln
            260                 265                 270

tct aaa tgt ttg cag gat aag atg act gct aaa gag agt gct acc tgg  1042
Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala Thr Trp
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        275                 280                 285

ctt gct att att aac caa gaa gag tcc ttg gct aga gag ctt tat ccc     1090
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    290                 295                 300

gag tca tgt cca cct ctt tct ctg tct ggt gga agt tgc tcg ctt ctg     1138
Glu Ser Cys Pro Pro Leu Ser Leu Ser Gly Gly Ser Cys Ser Leu Leu
305                 310                 315                 320

atg aat gat tgc agt caa tac gat gtt gaa ggt ttc gag aag gag tct     1186
Met Asn Asp Cys Ser Gln Tyr Asp Val Glu Gly Phe Glu Lys Glu Ser
                325                 330                 335

cac tat gaa gtg gaa gag ctc aag cca gaa aaa gtt atg aat tct tca     1234
His Tyr Glu Val Glu Glu Leu Lys Pro Glu Lys Val Met Asn Ser Ser
            340                 345                 350

aac ttt ggg atg gtt gct aaa atg cat gac ttt cct gtc aaa gaa gaa     1282
Asn Phe Gly Met Val Ala Lys Met His Asp Phe Pro Val Lys Glu Glu
        355                 360                 365

gtc cca gca gga aac tcg gaa ttc atg aga aag aga aag cca aac aga     1330
Val Pro Ala Gly Asn Ser Glu Phe Met Arg Lys Arg Lys Pro Asn Arg
    370                 375                 380

gat ctg aac act att atg gac aga acc gtt ttc acc tgc gag aat ctt     1378
Asp Leu Asn Thr Ile Met Asp Arg Thr Val Phe Thr Cys Glu Asn Leu
385                 390                 395                 400

ggg tgt gcg cac agc gaa atc agc cgg gga ttt ctg gat agg aat tcg     1426
Gly Cys Ala His Ser Glu Ile Ser Arg Gly Phe Leu Asp Arg Asn Ser
                405                 410                 415

aga gac aac cat caa ctg gca tgt cca cat cga gac agt cgc tta ccg     1474
Arg Asp Asn His Gln Leu Ala Cys Pro His Arg Asp Ser Arg Leu Pro
            420                 425                 430

tat gga gca gca cca tcc agg ttt cat gtc aat gaa gtt aag cct gta     1522
Tyr Gly Ala Ala Pro Ser Arg Phe His Val Asn Glu Val Lys Pro Val
        435                 440                 445

gtt gga ttt cct cag cca agg cca gtg aac tca gta gcc caa cca att     1570
Val Gly Phe Pro Gln Pro Arg Pro Val Asn Ser Val Ala Gln Pro Ile
    450                 455                 460

gac tta acg ggt ata gtt cct gaa gat gga cag aag atg atc tca gag     1618
Asp Leu Thr Gly Ile Val Pro Glu Asp Gly Gln Lys Met Ile Ser Glu
465                 470                 475                 480

ctc atg tcc atg tac gac aga aat gtc cag agc aac caa acc tct atg     1666
Leu Met Ser Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Ser Met
                485                 490                 495

gtc atg gaa aat caa agc gtg tca ctg ctt caa ccc aca gtc cat aac     1714
Val Met Glu Asn Gln Ser Val Ser Leu Leu Gln Pro Thr Val His Asn
            500                 505                 510

cat caa gaa cat ctc cag ttc cca gga aac atg gtg gaa gga agt ttc     1762
His Gln Glu His Leu Gln Phe Pro Gly Asn Met Val Glu Gly Ser Phe
        515                 520                 525

ttt gaa gac ttg aac atc cca aac aga gca aac aac aac aac agc agc     1810
Phe Glu Asp Leu Asn Ile Pro Asn Arg Ala Asn Asn Asn Asn Ser Ser
    530                 535                 540

aac aat caa acg ttt ttt caa ggg aac aac aac aac aac aat gtg ttt     1858
Asn Asn Gln Thr Phe Phe Gln Gly Asn Asn Asn Asn Asn Asn Val Phe
545                 550                 555                 560

aag ttc gac act gca gat cac aac aac ttt gaa gct gca cat aac aac     1906
Lys Phe Asp Thr Ala Asp His Asn Asn Phe Glu Ala Ala His Asn Asn
                565                 570                 575

aac aat aac agt agc ggc aac agg ttc cag ctt gtg ttt gat tcc aca     1954
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Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr
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ccg ttc gac atg gcg tca ttc gat tac aga gat gat atg tcg atg cca     2002
Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro
        595                 600                 605

gga gta gta gga acg atg gat gga atg cag cag aag cag caa gat gta     2050
Gly Val Val Gly Thr Met Asp Gly Met Gln Gln Lys Gln Gln Asp Val
    610                 615                 620

tcc ata tgg ttc taa agtcttggta gtagatttca tcttctctta tttttatctt     2105
Ser Ile Trp Phe
625

ttgtgttctt acattcactc aaccatgtaa tatttttttcc tgggtctctc tgtctctatc   2165

gcttgttatg atgtgtctgt aagagtctct aaaaactctc tgttactgtg tgtctttgtc   2225

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Pro Asp Ser Ile Val Glu Asp Asp Tyr Thr Asp Asp Glu Ile Asp Val
        35                  40                  45

Asp Glu Leu Glu Arg Arg Met Trp Arg Asp Lys Met Arg Leu Lys Arg
    50                  55                  60

Leu Lys Glu Gln Asp Lys Gly Lys Glu Gly Val Asp Ala Ala Lys Gln
65                  70                  75                  80

Arg Gln Ser Gln Glu Gln Ala Arg Arg Lys Lys Met Ser Arg Ala Gln
                85                  90                  95

Asp Gly Ile Leu Lys Tyr Met Leu Lys Met Met Glu Val Cys Lys Ala
            100                 105                 110

Gln Gly Phe Val Tyr Gly Ile Ile Pro Glu Asn Gly Lys Pro Val Thr
        115                 120                 125

Gly Ala Ser Asp Asn Leu Arg Glu Trp Trp Lys Asp Lys Val Arg Phe
    130                 135                 140

Asp Arg Asn Gly Pro Ala Ala Ile Thr Lys Tyr Gln Ala Glu Asn Asn
145                 150                 155                 160

Ile Pro Gly Ile His Glu Gly Asn Asn Pro Ile Gly Pro Thr Pro His
                165                 170                 175
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Thr Leu Gln Glu Leu Gln Asp Thr Thr Leu Gly Ser Leu Leu Ser Ala
180 185 190

Leu Met Gln His Cys Asp Pro Pro Gln Arg Arg Phe Pro Leu Glu Lys
195 200 205

Gly Val Pro Pro Pro Trp Trp Pro Asn Gly Lys Glu Asp Trp Trp Pro
210 215 220

Gln Leu Gly Leu Pro Lys Asp Gln Gly Pro Ala Pro Tyr Lys Lys Pro
225 230 235 240

His Asp Leu Lys Lys Ala Trp Lys Val Gly Val Leu Thr Ala Val Ile
245 250 255

Lys His Met Phe Pro Asp Ile Ala Lys Ile Arg Lys Leu Val Arg Gln
260 265 270

Ser Lys Cys Leu Gln Asp Lys Met Thr Ala Lys Glu Ser Ala Thr Trp
275 280 285

Leu Ala Ile Ile Asn Gln Glu Glu Ser Leu Ala Arg Glu Leu Tyr Pro
290 295 300

Glu Ser Cys Pro Pro Leu Ser Leu Ser Gly Gly Ser Cys Ser Leu Leu
305 310 315 320

Met Asn Asp Cys Ser Gln Tyr Asp Val Glu Gly Phe Glu Lys Glu Ser
325 330 335

His Tyr Glu Val Glu Glu Leu Lys Pro Glu Lys Val Met Asn Ser Ser
340 345 350

Asn Phe Gly Met Val Ala Lys Met His Asp Phe Pro Val Lys Glu Glu
355 360 365

Val Pro Ala Gly Asn Ser Glu Phe Met Arg Lys Arg Lys Pro Asn Arg
370 375 380

Asp Leu Asn Thr Ile Met Asp Arg Thr Val Phe Thr Cys Glu Asn Leu
385 390 395 400

Gly Cys Ala His Ser Glu Ile Ser Arg Gly Phe Leu Asp Arg Asn Ser
405 410 415

Arg Asp Asn His Gln Leu Ala Cys Pro His Arg Asp Ser Arg Leu Pro
420 425 430

Tyr Gly Ala Ala Pro Ser Arg Phe His Val Asn Glu Val Lys Pro Val
435 440 445

Val Gly Phe Pro Gln Pro Arg Pro Val Asn Ser Val Ala Gln Pro Ile
450 455 460

Asp Leu Thr Gly Ile Val Pro Glu Asp Gly Gln Lys Met Ile Ser Glu
465 470 475 480

Leu Met Ser Met Tyr Asp Arg Asn Val Gln Ser Asn Gln Thr Ser Met
485 490 495

Val Met Glu Asn Gln Ser Val Ser Leu Leu Gln Pro Thr Val His Asn
500 505 510

His Gln Glu His Leu Gln Phe Pro Gly Asn Met Val Glu Gly Ser Phe
515 520 525

Phe Glu Asp Leu Asn Ile Pro Asn Arg Ala Asn Asn Asn Asn Ser Ser
530 535 540

Asn Asn Gln Thr Phe Phe Gln Gly Asn Asn Asn Asn Asn Asn Val Phe
545 550 555 560

Lys Phe Asp Thr Ala Asp His Asn Asn Phe Glu Ala Ala His Asn Asn
565 570 575

Asn Asn Asn Ser Ser Gly Asn Arg Phe Gln Leu Val Phe Asp Ser Thr
580 585 590

Pro Phe Asp Met Ala Ser Phe Asp Tyr Arg Asp Asp Met Ser Met Pro
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Ser Ile Trp Phe
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Trp Thr Ser Glu Glu Asp Gln Lys Leu Val Asp Tyr Ile Gln Lys His
20 25 30

ggt tat ggt aac tgg aga acc ctc ccc aaa aat gcc ggt acg tgt ttg 144
Gly Tyr Gly Asn Trp Arg Thr Leu Pro Lys Asn Ala Gly Thr Cys Leu
35 40 45

caa aga tgt ggc aaa agt tgt agg tta agg tgg act aat tat ctc cga 192
Gln Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg
50 55 60

cca gat ata aaa cga gga aga ttc tct ttt gag gaa gaa gaa gcc att 240
Pro Asp Ile Lys Arg Gly Arg Phe Ser Phe Glu Glu Glu Glu Ala Ile
65 70 75 80

att cag ctt cat agc ttc tta gga aac aag tgg tct gcg att gcg gcg 288
Ile Gln Leu His Ser Phe Leu Gly Asn Lys Trp Ser Ala Ile Ala Ala

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cgt ttg cca gga aga aca gat aat gag atc aag aac ttt tgg aac act      336
Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Asn Thr
            100                 105                 110

cat ata aga aag aag cta ctt aga atg ggg att gat cca gtg act cac      384
His Ile Arg Lys Lys Leu Leu Arg Met Gly Ile Asp Pro Val Thr His
        115                 120                 125

agt cca cga ctc gat ctc ctc gat atc tca tcc atc tta gct tca tct      432
Ser Pro Arg Leu Asp Leu Leu Asp Ile Ser Ser Ile Leu Ala Ser Ser
    130                 135                 140

cta tac aat tca tct tca cat cac atg aac atg tca aga ctc atg atg      480
Leu Tyr Asn Ser Ser Ser His His Met Asn Met Ser Arg Leu Met Met
145                 150                 155                 160

gat act aat cgt cgt cat cag caa caa cat cca ttg gtt aac ccc gag      528
Asp Thr Asn Arg Arg His Gln Gln Gln His Pro Leu Val Asn Pro Glu
                165                 170                 175

ata ctc aag ctt gcg acc tct ata ttc tct caa aac caa aac caa aac      576
Ile Leu Lys Leu Ala Thr Ser Ile Phe Ser Gln Asn Gln Asn Gln Asn
            180                 185                 190

cac aac caa aat caa aac caa aac caa aac ctc gtg gtg gat cat gag      624
His Asn Gln Asn Gln Asn Gln Asn Gln Asn Leu Val Val Asp His Glu
        195                 200                 205

aag caa aca gtt tat cat cat cat gat gtt aac caa acc gga gta aac      672
Lys Gln Thr Val Tyr His His His Asp Val Asn Gln Thr Gly Val Asn
    210                 215                 220

caa tac caa acc gac caa tat ttc gag aac gcg att act caa gaa ctc      720
Gln Tyr Gln Thr Asp Gln Tyr Phe Glu Asn Ala Ile Thr Gln Glu Leu
225                 230                 235                 240

caa tct tcc atg cca cca ttc ccc aat gaa gct cat cag ttt aac gac      768
Gln Ser Ser Met Pro Pro Phe Pro Asn Glu Ala His Gln Phe Asn Asp
                245                 250                 255

atg gat cat cac ttc aat ggt ttt gga gaa caa aat ctt gtt tca act      816
Met Asp His His Phe Asn Gly Phe Gly Glu Gln Asn Leu Val Ser Thr
            260                 265                 270

tct act acg tca gtc caa gat tgc tat aat ccg tca ttc aac gat tat      864
Ser Thr Thr Ser Val Gln Asp Cys Tyr Asn Pro Ser Phe Asn Asp Tyr
        275                 280                 285

tca agt tca aat ttt gtc tta gat cat tct tat tcg gat cag agc ttc      912
Ser Ser Ser Asn Phe Val Leu Asp His Ser Tyr Ser Asp Gln Ser Phe
    290                 295                 300

aac ttc gca aat tcg gtc tta aac acg cca tcc tcg agc ccg agc ccg      960
Asn Phe Ala Asn Ser Val Leu Asn Thr Pro Ser Ser Ser Pro Ser Pro
305                 310                 315                 320

act acg tta aac tcg agt tac atc aat agt agc agt tgc agc act gag     1008
Thr Thr Leu Asn Ser Ser Tyr Ile Asn Ser Ser Ser Cys Ser Thr Glu
                325                 330                 335

gat gaa ata gaa agc tat tgc agt aat ctc atg aag ttt gat att ccc     1056
Asp Glu Ile Glu Ser Tyr Cys Ser Asn Leu Met Lys Phe Asp Ile Pro
            340                 345                 350

gat ttc ttg gac gtt aat ggt ttt att ata taa                        1089
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MBI-17 Sequence Listing.ST25

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Met Ala Arg Ser Pro Cys Cys Glu Lys Asn Gly Leu Lys Lys Gly Pro
1               5                  10                  15

Trp Thr Ser Glu Glu Asp Gln Lys Leu Val Asp Tyr Ile Gln Lys His
            20                  25                  30

Gly Tyr Gly Asn Trp Arg Thr Leu Pro Lys Asn Ala Gly Thr Cys Leu
        35                  40                  45

Gln Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg
    50                  55                  60

Pro Asp Ile Lys Arg Gly Arg Phe Ser Phe Glu Glu Glu Glu Ala Ile
65                  70                  75                  80

Ile Gln Leu His Ser Phe Leu Gly Asn Lys Trp Ser Ala Ile Ala Ala
                85                  90                  95

Arg Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Asn Thr
            100                 105                 110

His Ile Arg Lys Lys Leu Leu Arg Met Gly Ile Asp Pro Val Thr His
        115                 120                 125

Ser Pro Arg Leu Asp Leu Leu Asp Ile Ser Ser Ile Leu Ala Ser Ser
    130                 135                 140

Leu Tyr Asn Ser Ser Ser His His Met Asn Met Ser Arg Leu Met Met
145                 150                 155                 160

Asp Thr Asn Arg Arg His Gln Gln Gln His Pro Leu Val Asn Pro Glu
                165                 170                 175

Ile Leu Lys Leu Ala Thr Ser Ile Phe Ser Gln Asn Gln Asn Gln Asn
            180                 185                 190

His Asn Gln Asn Gln Asn Gln Asn Gln Asn Leu Val Val Asp His Glu
        195                 200                 205

Lys Gln Thr Val Tyr His His His Asp Val Asn Gln Thr Gly Val Asn
    210                 215                 220

Gln Tyr Gln Thr Asp Gln Tyr Phe Glu Asn Ala Ile Thr Gln Glu Leu
225                 230                 235                 240

Gln Ser Ser Met Pro Pro Phe Pro Asn Glu Ala His Gln Phe Asn Asp
                245                 250                 255

Met Asp His His Phe Asn Gly Phe Gly Glu Gln Asn Leu Val Ser Thr
            260                 265                 270

Ser Thr Thr Ser Val Gln Asp Cys Tyr Asn Pro Ser Phe Asn Asp Tyr
        275                 280                 285
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MBI-17 Sequence Listing.ST25

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Ser Ser Ser Asn Phe Val Leu Asp His Ser Tyr Ser Asp Gln Ser Phe
    290                 295                 300

Asn Phe Ala Asn Ser Val Leu Asn Thr Pro Ser Ser Ser Pro Ser Pro
305                 310                 315                 320

Thr Thr Leu Asn Ser Ser Tyr Ile Asn Ser Ser Ser Cys Ser Thr Glu
                325                 330                 335

Asp Glu Ile Glu Ser Tyr Cys Ser Asn Leu Met Lys Phe Asp Ile Pro
            340                 345                 350

Asp Phe Leu Asp Val Asn Gly Phe Ile Ile
        355                 360
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INTERNATIONAL SEARCH REPORT

Intern...al application No.

PCT/US00/31457

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : A01H 1/00, 5/00; A61K 38/10; C07H 21/00; C12N 5/14, 15/11, 15/29, 15/82

US CL : 435/468,419,320.1;530/300,326,327;536/23.1,23.6;800/278,281,287,305-310,314,315,317.1-317.4,320.1-320.3

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/468,419,320.1;530/300,326,327;536/23.1,23.6;800/278,281,287,305-310,314,315,317.1-317.4,320.1-320.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EAST, STN (Agricola, Biosis, Caplus, Embase), SEQ ID NO: 1&2

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X --- Y	LI, S.F. et al. A novel myb-related gene from Arabidopsis thaliana. FEBS Letters 1996, Vol. 379, pages 117-121, entire reference	1-14, 25 & 26 --- 27
X --- Y	SCHAFFER, R. et al. The late elongated hypocotyl mutation of Arabidopsis disrupts circadian rhythms and the photoperiodic control of flowering. Cell 1998, Vol. 93, pages 1219-1229.	1-14, 25 & 26 --- 27
Y	Database NCBI Nucleotide, U.S. National Library of Medicine, (Bethesda, MD, USA), No. U28422, WANG, Z. Direct Submission, Sequence, January 14, 1997.	1-14 & 25-27
Y	US 5,939,601 (KLESSIG et al) 17 August 1999 (17.08.1999), entire reference.	1-14 & 25-27
Y	SUZUKI, A. et al. Cloning and expression of five myb-related genes from rice seed. Gene 1997, Vol. 198, pages 393-398.	1-14 & 25-27
Y,P	LOGUERCIO, L.L. et al. Differential regulation of six novel myb-domain genes defines tow distinct expression patterns in allotetraplid cotton (Goxxypium hirsutum L.), Mol. Gen. Genet. 1999, Vol. 261, pages 660-671.	1-14 & 25-27
Y,P	KIRIK, V. et al. Two novel myb homologues with changed expression in late embryogenesis-defective Arabidopsis mutants. Plant Mol. Biol. 1998, Vol. 37, pages 819-827.	1-14 & 25-27

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
14 February 2001 (14.02.2001)	19 MAR 2001
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer David Kruse Telephone No. 703-308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

Int[illegible]onal application No.
PCT/US00/31457

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-14 &25-27:SEQ ID NOs: 1&2

Remark on Protest
☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Int ional application No.
PCT/US00/31457

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Groups I-XXVII, claim(s) 1-14 and 25-27, drawn to a transgenic plant having modified seed characteristics, polynucleotides and vectors for producing said transgenic plant and a method of making said transgenic plant. Applicant must elect one pair of sequences (one nucleic acid and the corresponding amino acid translation) to be examined, *i.e.* SEQ ID NO: 1 and 2 in Group I, SEQ ID NO: 3 and 4 in Group II, SEQ ID NO: 5 and 6 in Group III, etc.

Group XXVIII, claim(s) 15-17, drawn to a method of identifying a factor that is modulated.

Group XXIX, claims(s) 18, drawn to a method of identifying a molecule that modulates activity or expression of a polynucleotide or polypeptide.

Group XXX, claims(s) 19 and 20, drawn to an integrated computer system.

Group XXXI, claim(s) 21-24, drawn to a method for identifying a polynucleotide sequence comprising selecting a nucleic acid sequence from a database that meets a selected sequence criteria.

The inventions listed as Groups I-XXXI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The inventions listed as Groups I-XXXI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Groups I-XXVII are drawn to a transgenic plant and a method of producing said plant with a nucleic acid sequence. The methods of Groups I-XXVII differ from each other in that they are directed to a plant transformation method and transgenic plant with a structurally and functionally distinct nucleic acid sequence which encodes a structurally and functionally distinct amino acid sequence. In addition, Groups XXVIII, XXIX and XXXI are different methods from any of Groups I-XXVII in that they have different method steps and different end products, and Group XXX requires a computer system. Thus, there is no single special technical feature, which links the inventions of Groups I-XXXI under PCT Rule 13.2.